

Best Local Similarity 34.2%; Pred. No. 1.2e-19;  
 Matches 64; Conservative 48; Mismatches 64; Indels 11; Gaps 3;  
 Residues: 1-254 <ESCS>  
 A;Accession: PD0018  
 A;Molecule type: protein  
 F;Residues: 1-254 <ESCS>  
 C;Superfamily: ricin; RNA N-glycosidase homology  
 F;7-246/Domain: rRNA N-glycosidase homology <RNG>

Query 10 INFITAGATVSYTINFIARVGRGTTGADYHEIPVLPNRVGLPINOREFLVLELSNHAEL 69  
 Database 3 VSFSLGADSKEKSYSKPITALRKALPSKEKSNIPILPSSGA --SRVLMQTSNYDAK 59

Query 70 SVTIALDVNTAYVVGYRAGNSAYFPHPDNEAFAITHLTDFDQNRYTAFFGGNYDRLEQ 129  
 Database 60 AITMAIDTVNVYTMGYLNNTSYF --ANESDKLAKASQVFKGSTLVITPYSENTERLQN 116

Query 130 LAGNLRENTENGGPYLEAISALYYSTGGTQLPLPALARFCIQMISEARAFQXIEGEM 189  
 Database 117 AAGKIREKIPUGFRALDSALTSIHYDS --TAAAAALVLVLOTTAASRFKXIEGQI 171

Query 190 RTRIRYN 196  
 Database 172 IERIPRN 178

RESULT 14

S62627 Glutinin I precursor - European elder  
 C;Species: Sambucus nigra (European elder)  
 C;Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Aug-1999

C;Accession: S62627; S62619  
 Ryan Dianne, E.J.M.; Barre, A.; Rouge, P.; van Leuven, F.; Peumans, W.J.

Eur. J. Biochem., 235, 128-137, 1996  
 A;Title: The NeuAc(alpha-2,6)-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)

A;Reference: S62619; PMID:86202926; PMID:8631319  
 A;Accession: S62627  
 A;Status: preliminary

A;Molecule type: mRNA  
 A;Residues: 1-70 <VAN>

A;Cross-references: EMBL:U27122; PIDN: AAC49158.1; PID: g1141773  
 A;Accession: S62619

A;Status: preliminary

A;Molecule type: protein  
 A;Residues: 29-39;309-319 <VAN>

C;Superfamily: ricin; rRNA N-glycosidase homology <RNG>

F;37-283/Domain: rRNA N-glycosidase homology <RNG>

Query Match 28.3%; Score 291; DB 2; Length 570;  
 Matches 76; Conservative 33; Mismatches 74; Indels 12; Gaps 6;

Query 2 IFPKQYPIINFATAGVSYTINFIARVGRGTTGADYHEIPVLPNRVGLPINOREFLV 61  
 Database 29 VTPPPVTPSVFNLUTGA -DTIEPFLRQLEKVTILGNHTAFLPVNPESQVDSNRFVLV 86

Query 62 ELSNHAEASVTLALDVNTAYVVGYRAGNSAYFPHPDNEAFAITHLTDFDQNRYTAFF 119  
 Database 87 PTINPSCDPTVTAIDVNYLYVAFSSNGKSYFSGSTAVQRD---NLFTD-TDELN 140

Query 120 FGGNYDRLQGLGNLRENIELGGPYLEAISALYYYS TGGTQLPTLARSFLICIONMISE 178  
 Database 141 FCTCNYTSIHERQFGFRYVLPQPKSLDQAISSRTVLTAGTKP-LARGLIVIVQVE 199

Query 179 ARFQYIEGEMTRI 193  
 Database 200 ARFRYIELRRTSI 214

RESULT 15

PD0018 mistletoe lectin I A chain - Viscum album (fragment)

C;Species: Viscum album

C;Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 26-Aug-1999

C;Accession: PD0018

R;Eschenburg, S.; Krausenhaar, R.; Mikhailov, A.; Stoeva, S.; Betz, C.; Voelter, W.

Biochem. Biophys. Res. Commun., 247, 367-372, 1998

A;Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum albu

A;Reference number: PD0018; PMID:98308123; PMID:9642133

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1024	RICCI_RICCO	576	1	RICCI_RICCO	P02879	ricinus com
2	914.5	AGGL_RICCO	564	1	AGGL_RICCO	P06750	ricinus com
3	352.5	ABRB_ABRPR	562	1	ABRB_ABRPR	P28590	abrus preca
4	345	ABRB_ABRPR	527	1	ABRB_ABRPR	Q06077	abrus preca
5	342	RIP1_TRIXI	289	1	RIP1_TRIXI	P09989	trichosanth
6	341.5	RIP2_BRYDI	282	1	RIP2_BRYDI	P98184	bryonia dio
7	338	RIPS_TRICKI	289	1	RIPS_TRICKI	P24478	trichosanth
8	330.5	NIGB_SANNI	563	1	NIGB_SANNI	P33183	sambucus ni
9	329.5	ABRA_ABRPR	528	1	ABRA_ABRPR	P11140	abrus preca
10	312	RIP1_BRYDI	290	1	RIP1_BRYDI	P33185	bryonia dio
11	300	RIP2_LUFETY	250	1	RIP2_LUFETY	P22851	luffa cylindrica
12	296.5	RIP1_CUCFI	286	1	RIP1_CUCFI	Q9FRX4	cucumis sativus
13	286	MLA_VISAL	278	1	MLA_VISAL	P81446	viscum album
14	284.5	RIP1_LUFCY	277	1	RIP1_LUFCY	P00465	luffa cylindrica
15	279	RIP2_MOMBA	286	1	RIP2_MOMBA	P29339	momordica balsamina
16	277	RIP1_MOMCH	286	1	RIP1_MOMCH	P16094	momordica charantia
17	260	RIP1_TRITAN	294	1	RIP1_TRITAN	P56626	trichosanth
18	245.5	RIP2_GELMU	239	1	RIP2_GELMU	P3186	gelenium mucronatum
19	197.5	RIP1_PHYAM	316	1	RIP1_PHYAM	P01464	phytolacca
20	182	RIP1_PHYAM	277	1	RIP1_PHYAM	P10297	phytolacca
21	180.5	RIP2_PHYAM	313	1	RIP2_PHYAM	P23339	phytolacca
22	178	RIP1_MIRJU	261	1	RIP1_MIRJU	P23326	mirabilis jalapa
23	140	RIP2_HORVU	278	1	RIP2_HORVU	P03399	hordeum vulgare
24	133	RIP1_HORVU	280	1	RIP1_HORVU	P22244	hordeum vulgare
25	131	RIP1_SAEOF	253	1	RIP1_SAEOF	Q14391	saponaria officinalis
26	127	RIP5_SAEOF	253	1	RIP5_SAEOF	Q41389	saponaria officinalis
27	126	RIP2_DHYAM	310	1	RIP2_DHYAM	Q40772	phytolacca
28	124	RIP6_SAEOF	121	1	RIP6_SAEOF	P20556	saponaria officinalis
29	123.5	RIP1_DIACA	293	1	RIP1_DIACA	P24476	dianthus carthusianorum
30	121	RIP2_SAEOF	292	1	RIP2_SAEOF	P27559	saponaria officinalis
31	111	RIP3_SAEOF	319	1	RIP3_SAEOF	P27560	saponaria officinalis
32	110	RIP3_MAIZE	236	1	RIP3_MAIZE	P25891	zea mays (m
33	109.5		428	1	ENO_NEIMA		

"Ricin." LT Toxicon 39:1723-1728 (2001).

[8] X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS). MEDLINE=B715983; PubMed=3553397; Monfort W., Viallaffranca J.E., Monzingo A.F., Ernst S.R., Katzin B., Rutherford E., Xiong N.H., Hamlin R., Robertus J.D.; "The three-dimensional structure of ricin at 2.8 A." ; J. Biol. Chem. 262:3398-3403 (1987).

[9] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN. MEDLINE=91352004; PubMed=1881881; Katzin B.J., Collins E.J., Robertus J.D.; Rutherford E., "Structure of ricin A-chain at 2.5 A." ; Proteins 10:251-259 (1991).

[10] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN. MEDLINE=91352005; PubMed=1881882; Rutherford E., Robertus J.D.; "Structure of ricin B-chain at 2.5-A resolution." ; Proteins 10:260-269 (1991).

[11] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN. MEDLINE=91352010; PubMed=1990130; Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J., Paupitz R.A.; "X-ray structure of recombinant ricin A-chain at 1.8-A resolution." ; J. Mol. Biol. 244:410-422 (1994).

[12] X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215. MEDLINE=96374222; PubMed=780513; Day P.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M., Molina-Svintis M.C., Robertus J.D.; "Structure and activity of an active site substitution of ricin A chain." ; Biochemistry 35:11098-11103 (1996).

[13] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN. MEDLINE=97240820; PubMed=9086288; Yan X., Hollis T., Svintis M., Day P., Monzingo A.F., Milne G.W., Robertus J.D.; "Structure-based identification of a ricin inhibitor." ; J. Mol. Biol. 266:1043-1049 (1997).

[14] MUTAGENESIS. MEDLINE=93165632; PubMed=1287657; Kin Y., Robertus J.D.; "Analysis of several key active site residues of ricin A chain by mutagenesis and X-ray crystallography." ; Protein Eng. 5:775-779 (1992).

-!- FUNCTION: Ricin is highly toxic to animal cells and to a less extent to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal subunits. It acts as a glycosidase that removes a specific adenine residue from an exposed loop of 28S ribosomal RNA. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein synthesis. Thus the A chain can inactivate a few thousand ribosomes per minute, thus inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity). It binds to beta-D-galactopyranoside moieties.

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenose on the 28S rRNA.

-!- SUBUNIT: Disulfide-linked dimer of A and B chains.

-!- DOMAIN: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).

-!- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.

-!- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-INTERACTING PROTEIN FAMILY, TYPE 2 RIP SURPAMITY.

-|- SIMILARITY: Contains 2 ricin B-type lectin domains.

-|- CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).

-|- DATABASE: NAME=Protein Spotlight; NOTE=Issue 31 of February 2003; WWW=<http://www.exasy.org/spotlight/articles/spt1031.html>.

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CC	DR	X52908;	CAA37095.1;	-.
CC	DR	X52908;	CAA37095.1;	-.
CC	EMBL	X02388;	CAA26230.1;	-.
CC	EMBL	X02388;	CAA26230.1;	-.
CC	DR	A12832;	CAA01058.1;	-.
CC	DR	P13179;	CRA26939.1;	-.
CC	DR	X52908;	CAA37095.1;	-.
CC	DR	X52908;	CAA37095.1;	-.
CC	DR	A24041;	RUCSD.	
CC	DR	ZAAI;	31-JAN-94.	
CC	DR	IAPG;	31-JAN-94.	
CC	DR	IFMP;	31-OCT-93.	
CC	DR	LIFS;	14-JAN-98.	
CC	DR	LIFT;	14-JAN-98.	
CC	DR	LIIFU;	14-JAN-98.	
CC	DR	IRTC;	31-OCT-93.	
CC	DR	IOBS;	16-JUN-97.	
CC	DR	IBOT;	16-JUN-97.	
CC	DR	IBRS;	02-SEP-98.	
CC	DR	IBR6;	02-SEP-98.	
CC	DR	IL1L3;	16-JAN-02.	
CC	DR	IL1L4;	16-JAN-02.	
CC	DR	IL1L9;	16-JAN-02.	
CC	DR	Glycosidases;	P02879;	-.
CC	DR	InterPro;	IPR000722; Ricin_B_lectin.	
CC	DR	InterPro;	IPR001574; RIP.	
CC	DR	PF00654;	Ricin_B_lectin;	6.
CC	DR	PF00161;	RIP;	1.
CC	DR	PR00396;	SHIGARICIN.	
CC	DR	SMART;	SM00458;	RICIN; 2.
CC	DR	PROSITE;	PS00231; RICIN_B_LECTIN;	2.
CC	DR	PROSITE;	PS00275; SHIGA_RICIN;	1.
CC	KW	Plant defense;	Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;	
CC	KW	Glycoprotein; Lectin; Signal;	3D-structure.	
FT	SIGNAL	1	35	
FT	CHAIN	36	302	RICIN_A_CHAIN.
FT	PEPTIDE	303	314	LINKER PEPTIDE.
FT	CHAIN	315	576	RICIN_B_CHAIN.
FT	DOMAIN	321	448	RICIN_B-TYPE LECTIN 1.
FT	DOMAIN	451	575	RICIN_B-TYPE LECTIN 2.
FT	REPAT	331	373	1-ALPHA.
FT	REPAT	374	414	1-BETA.
FT	REPAT	417	449	1-GAMMA.
FT	REPAT	462	497	2-ALPHA.
FT	REPAT	501	540	2-BETA.
FT	REPAT	543	570	2-GAMMA.
FT	ACT_SITE	212	212	INTERCHAIN.
FT	DISTRIFID	294	318	
FT	DISTRIFID	334	353	
FT	DISTRIFID	377	394	
FT	DISTRIFID	465	478	N-LINKED (GLCNAC. . .).
FT	DISTRIFID	504	521	/FTG=CAR 000000.
FT	CARBHYD	45	45	N-LINKED (GLCNAC. . .) (IN MINOR FORM).
FT	CARBHYD	271	271	/FTG=CAR 000001.
FT	CARBHYD	409	409	N-LINKED (GLCNAC. . .).
FT	CARBHYD	449	449	N-LINKED (GLCNAC. . .).
FT	CONFLECT	76	76	B -> D (IN REF. 3).
FT	CONFLECT	551	551	A -> R (IN REF. 3).
FT	STRAND	47	49	
FT	TURN	49	50	

Query Match Score 99.5%; Score 1024; DB 1; Length 576;  
 Best Local Similarity 100.0%; Pred. No. 1.e-87; Mismatches 0; Indels 0; Gaps 0;  
 Matches 199; Conservative 0; Mismatches 0;

Qy 2 IPKQPIINFTAGATVQSYTNFIRAVGRLLTGADRVHEIPVLFNRLVGLPINQRFLIV 61  
 Db 36 IPKQPIINFTAGATVQSYTNFIRAVGRLLTGADRVHEIPVLFNRLVGLPINQRFLIV 95

Qy 62 EISNHAEVLSTVIALDVTINAYVGYRAGNSAAYFHPDNQEDAATIHLFTDVQNRITFAFG 121  
 Qy 96 EISNHAEVLSTVIALDVTINAYVGYRAGNSAAYFHPDNQEDAATIHLFTDVQNRITFAFG 155

Db 122 GNYDRLEQLAGNLRENLGNCPLERAISALYYXYSNGTQLPTLARSFICOMISEAAR 181  
 Db 156 GNYDRLEQLAGNLRENLGNCPLERAISALYYXYSNGTQLPTLARSFICOMISEAAR 215

Qy 182 FQYIEGMRTRIYNRSA 200  
 Db 216 FQYIEGMRTRIYNRSA 234

RESULT 2

ID	AGGL_RICCO	STANDARD	ERT	564 AA.
AC	PE06750;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DB	Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-S glycosidase) (EC 3.2.2.22); Agglutinin B chain].			
OS	Ricinus communis (Castor bean).			
OS	Karyophyllales; Spermatophytina; Embryophytina; Tracheophytina; Spermatophytina; Viridiplantae; Magnoliophytina; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.			
RN	[1] - SEQUENCE FROM N.A. MEDLINE=86159449; PubMed=299130; [2] - RA Roberts L.M.; Lamb F.I.; Pappin D.J.C.; Word J.M.; RT "The primary sequence of Ricinus communis agglutinin. Comparison with ricin."; RL J. Biol. Chem. 260:15682-15686 (1985). RN SEQUENCE OF 303-564.			
RP	RC TISSUE-Seed; RA Araki T.; Yoshioka Y.; Funatsu G.; RT "The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds."; RL RNA RP SEQUENCE OF 303-337. RX MEDLINE=10178723; PubMed=6768555; RA Lin T.-S.; Li S.-L.; RT "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis"; RL Eur. J. Biochem. 105:453-459 (1980). CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA. CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY. CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).			
DR	M12099; AAA33869.1; -; EMBL; S40368; AAB22584.1; -.			

DR PIR: A24261; RLCSAG.  
 DR HSSP; P02879; 1BRG.  
 DR GlycoDB; P06750; -.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF001652; Ricin\_B\_lectin; 6.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR SMART; SM0458; RICIN; 2.  
 DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.

FT SIGNAL; 1 24

FT CHAIN 25 290

FT PROPEP 291 302

FT CHAIN 303 564

FT DOMAIN 309 436

FT DOMAIN 439 563

FT REPEAT 319 361

FT REPEAT 362 402

FT REPEAT 405 437

FT REPEAT 450 485

FT REPEAT 489 528

FT REPEAT 531 558

FT ACT SITE 200 200

FT DISULFID 282 306

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FT CARBONYL 34 34

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**Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyra;**  
**Spermatophytina; Magnoliophyta; euicotsyledons; core eudicots; Rosidae;**  
**eurosid I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.**  
 NCBI\_TaxID=316;  
 [1]  
 SEQUENCE FROM N.A.  
 RP  
 TISSUE=leaf;  
 MEDLINE=91266957; PubMed=2050149;  
 Wood K.A., Lord J.M., Nawrzynicz E.J., Piatrak M.;  
 "Preproabrin: Genomic cloning, characterisation and the expression of  
 the A-chain in Escherichia coli";  
 Eur. J. Biochem. 198:723-732 (1991).  
 -1- FONCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN  
 SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL  
 SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28S RNA. THE  
 B CHAIN IS A GLUCOSE-SPECIFIC LECTIN THAT FACILITATES THE  
 BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.  
 -1- CATALYTIC ACTIVITY: Endohydrolysis of  
 specific adenosine on the 28S rRNA.  
 -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
 -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN  
 CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
 -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-  
 INACTIVATING PROTEIN-FAMILY. TYPE 2 RIP SUBFAMILY.  
 -1- SIMILARITY: Contains 2 ricin B-type lectin domains.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

Best Local Similarity	45.5%	Pred. No.	2-6e-25;	Indels	9;	Gaps	4;
Matches	86;	Conservative	24;	Mismatches	70;		
Dy							
Dy	6	QYPIINFFTAGATVOSTYNTRAVRGRLTGADYRHEIPYLPNRYGLPINQNRFLFILVELSN	65				
Dy	35	QDQYKTFKTEGASQSQYKOFIEALRQLRTG--LHDIPVLPDPITVEERNRYTVELSN	92				
Dy	66	HAEELSVTLADVTNAVVYGRAGNSAYFFHPDNQEDAEATHLFITVQNYTFAFGNGYD	125				
Dy	93	SERESIEVGIDVTNAVVYARAGSOSYFL--RDAPASASTYLFPTQ--RYSLRFLDSYG	148				
Dy	126	RLEQAGLNRLNIEBINGPLEEAISALAYYSTGGTQLPTLARSFCIQMSEARQQYI	185				
Dy	149	DLEEWAHQTREEISLQLALTHAIS--FLRSGASMDEEKARTLIVIIQMASEAARYYI	205				
QY	186	EGENRTRIR	194				
Dy	206	SNRGSVSI	214				

PRESIDENT 4

RECCHI 1

STANDARD:

006077: D81374: CHINESE; 1955- ;

THE JOURNAL OF CLIMATE

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Query Match Score 345; DB 1; Length 527;  
 Best Local Similarity 45.5%; Pred. No. 1.5e-24;  
 Matches 87; Conservative 22; Mismatches 10; Gaps 4;

6 QYPIINFTAGATVOSYTNTFIRAVGRGLTCAADVREHIPVLPNRYGLPINQRFLIVELSN 65  
 1 QDQVQKPFTEATSQSYKQFFEARLQLTGG--LHGIPVLPDPTTLQERNRYISVELSN 58

66 HAEELSVTLALLDTNAVYVGAGNSAYFFHDNQEDAEATLFLFTDVQNYTFAGGGNYD 125  
 59 SDTESTEAGIIVSNATVVAEAGNRSYFL---RDAFTSASRYLFTCTQ-QVSLRFNGSYI 114

Qy 126 FLEQLQNLRLNIELGNGPLEBAISALYYSTGGTQPLTALSFSFTICOMSEARFQYI 185  
 Db 115 DLERLAROTRQOPIGLQALRAISEL---QSQTDDQEARTLIVLIVQWASEARYRFI 170

Qy 186 EGEMLTRIYN 196  
 Db 171 SYRGVGSIRTN 181

RIPT\_TRIKI STANDARD; PRT; 289 AA.  
 ID \_RIPT\_TRIKI AC  
 AC P09985; DT 01-MAR-1989 (Ref. 10, Created)  
 DR 01-NOV-1990 (Ref. 16, Last sequence update)  
 DR 15-SEP-2003 (Ref. 42, Last annotation update)  
 DE Ribosome-inactivating protein alpha-trichosanthin precursor  
 DE (rRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).  
 OS Trichosanthis kirilowii (Mongolian snake-gourd).  
 OC Lukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Embryophyta; Trichosanthis  
 OC eudicots; Rosidae; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 OX NCBI\_TaxID:3677;  
 RN [1]  
 RN PRT FROM N.A.;  
 RC SEQUENCE FROM N.A.; TISSUE=Leaf;  
 RC MEDLINE=91153657; PubMed=199291;  
 RX RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;  
 RT "Cloning of trichosanthin cDNA and its expression in Escherichia  
 coli";  
 RT Gene 97:267-272(1991).  
 RN [2]  
 RN PRT FROM N.A.; TISSUE=Tuberous root;  
 RC SEQUENCE FROM N.A.; TISSUE=Root;  
 RC MEDLINE=90256790; PubMed=2341400;  
 RX RA Chow T., Feldman R.A., Lovett M., Piatak M.;  
 RA "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a  
 type I ribosome-inactivating protein.";  
 RL J. Biol. Chem. 265:8670-8674(1990).  
 RN [3]  
 RN PRT SEQUENCE OF 24-270;  
 RC STRAIN=Maximowicz; PubMed=1341399;  
 RX MEDLINE=90256789; PubMed=2341399;  
 RA Collins B.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,  
 RA Wu P., Hwang K., Piatak M.;  
 RA "Primary amino acid sequence of alpha-trichosanthin and molecular  
 models for abrin A-chain and alpha-trichosanthin.";  
 RL J. Biol. Chem. 265:8665-8669(1990).  
 RN [4]  
 RN PRT SEQUENCE OF 24-270;  
 RC TISSUE=Tuberous root;  
 RA Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,  
 RA Tian G.Y., Ni C.Z.;  
 RA "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and  
 application";  
 RT Pure Appl. Chem. 58:789-798(1998).  
 RL [5]  
 RN PRT X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).  
 RX MEDLINE=94344957; PubMed=8066085;  
 RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;  
 RA "Structure of trichosanthin at 1.88-A resolution.";  
 RT Proteins 19:4-13(1994).  
 RL [6]  
 RN PRT X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE=95344383; PubMed=7659070;  
 RT "Studies on crystal structures, active-centre geometry and  
 depurinating mechanism of two ribosome-inactivating proteins.";  
 RL Biochem. J. 309:285-298(1995).  
 CC -- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS  
 CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT  
 INACTIVATES EUKARYOTIC 40S RIBOSOMAL SUBUNITS.  
 CC -- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenine on the 28S rRNA.  
 CC -- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC -- TYPE 1 RIP SUBFAMILY.

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 modified and this statement is not removed. Usage by and for commercial  
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or send an email to license@isb-sib.ch).

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CC EMBL; M34558; AAA34207.1; -.

CC EMBL; J05334; AAA34206.1; -.

DR PIR; JT0566; RLI7ZT.

DR PDB; 1MRJ; 07-FEB-95.

DR PDB; 1MRK; 07-FEB-95.

DR PDB; 1TCB; 10-JUL-95.

DR PDB; 1U4G; 28-JAN-03.

DR PDB; 1NL1; 21-JAN-03.

DR PDB; 1QD2; 14-APR-00.

DR InterPro; IPR01574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PRO0396; SHIGARICIN.

DR Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;

KW Toxin; Signal; 3D-structure.

FT SIGNAL 1 23

FT CHAIN 24 270 RIBOSOME-INACTIVATING PROTEIN ALPHA-TRICHOSANTHIN.

FT PROPEP 271 289 MISSING IN MATURE PROTEIN.

FT ACT SITE 183 183 BY SIMILARITY.

FT CONFLICT 57 60 TPPL -> LPPL (IN REF. 4).

FT CONFLICT 82 84 MISSING (IN REF. 4).

FT CONFLICT 87 87 I -> L (IN REF. 4).

FT CONFLICT 92 92 V -> VDAGLPPNAVL (IN REF. 4).

FT CONFLICT 143 144 KI -> GL (IN REF. 4).

FT CONFLICT 196 196 K -> S (IN REF. 4).

FT CONFLICT 215 216 WS -> LWL (IN REF. 4).

FT CONFLICT 231 231 Q -> T (IN REF. 4).

FT CONFLICT 234 234 S -> T (IN REF. 2).

FT CONFLICT 246 266 MISSING (IN REF. 4).

FT CONFLICT 247 247 T -> M (IN REF. 2).

FT STRAND 25 28

FT TURN 30 31

FT HELIX 34 46

FT TURN 47 47

FT STRAND 50 54

FT TURN 55 56

FT STRAND 57 60

FT HELIX 66 69

FT STRAND 70 76

FT TURN 78 79

FT STRAND 82 88

FT TURN 89 92

FT STRAND 93 99

FT TURN 100 101

FT SPRAND 102 105

FT HELIX 109 114

FT TURN 115 117

FT TURN 120 121

FT STRAND 124 127

FT HELIX 134 141

FT TURN 142 142

FT HELIX 145 147

FT STRAND 150 150

FT HELIX 152 163

FT TURN 164 165

FT HELIX 167 180

FT TURN 181 181

FT HELIX 182 186

FT STRAND 187 187

FT HELIX 188 195

FT TURN 196 196

FT STRAND 202 202

FT HELIX 206 226

FT TURN 227 230

FT STRAND 231 239

FT TURN 242 242

FT STRAND 245 250

FT TURN 251 252

FT HELIX 254 258

FT TURN 259 259

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FT STRAND 260 260

FT STRAND 263 263

FT TURN 268 268

FT SEQUENCE 289 AA; 31676 MW; 5CB09BB63057BB9 CRC64;

Query Match 33.2%; Score 342; DB 1; Length 289;

Best Local Similarity 39.5%; Pred. No. 1.4e-24;

Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps 5;

QY 10 INFITAGATVQSYTNEFIRAVGRGLTGDYVREIPVLPVRGLPINQRTFLVLSNHAEI 69

Db 25 VSFRUSGAISSSGYFISNRKALPNERK-LYDPLL-RSSLPGSQRTALIHLTNAYDE 81

QY 70 SVTLALDVITNAYVGYRAGNSAYFFFHDNOEDA-BATHLIFTDQNRTFAGGNYDRLE 128

Db 82 TISVADIVINVIMSYRAGDTSYFF--NEASATEAKVYKDAMRKVTPSGMYERLQ 138

QY 129 QLAGNIRENTLGNGPLEBARISALYYSTGGTOL-PTLARSFIICIQMISAAFRFOYIEGE 188

Db 139 TAAGKIRENTPLGLPDLSDATTLYNNAN---SAASALMVLIQSTSEARYKPFQQ 193

---

RESULT 6

RIP2\_BRYDI STANDARD; PRT; 282 AA.

ID RIP2\_BRYDI STANDARD; PRT; 282 AA.

AC P98184; Q988U0; RA Siegall C.B., Gawlik S.L., Marquardt H.; RT "Bryodin 2, a ribosome-inactivating protein bryodin II precursor (rRNA N- glycofidae)" (EC 3.2.2.22) (B92).

DT 16-OCT-2001 (Rel. 40, Last sequence update) DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT Ribosome-inactivating protein bryodin II precursor (rRNA N- glycofidae) (EC 3.2.2.22) (B92).

OS Bryonia dioica (Red bryony). CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; OC eurosids I; Cucurbitales; Cucurbitaceae; Bryonia. OC NCBI\_TAXID=3652;

OX RN SEQUENCE FROM N.A. [1]

RN SEQUENCE FROM N.A. [2]

RA Siegall C.B., Gawlik S.L., Marquardt H.; RT "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunoenconjugates"; RT Bryonia dioica 2, a ribosome-inactivating protein bryodin 2, RT Bryonia dioica.; RT Patent number US5597569, 28-JAN-1997.

RL RPT SEQUENCE OF 22-42.

RN RN TISSUE Root; RX MEDLINE=951511812; PubMed=7849072; RA Marquardt H.; RA Siegall C.B., Gawlik S.L., Chace D., Wolff E.A., Mixan B., RT "Protein synthesis in animal cells (by similarity)." CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one CC specific adenosine on the 28S rRNA. CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. CC TYPE 1 RIP SUBFAMILY.

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CC DR EMBL; I34238; ; NOT\_ANNOTATED\_CDS. CC HSSP; P09989; 1M RJ.

DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PRO0396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA RICIN; 1.  
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;  
 KW Multigene family; Glycoprotein signal.

FT SIGNAL 1 21 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.  
 FT CHAIN 22 202 BY SIMILARITY.  
 FT ACT SITE 183 183 N-LINKED (GlycNAc. . .) (POTENTIAL).  
 FT CARBOHYD 25 25 MW: C52B2F26A73769C CRC64;  
 SQ SEQUENCE 282 AA; 30754 MW;

Query Match 10 INFTTAGATVQSYNTNFIRAVRGRLLTGADVRHEIPVLPN-RVGLPINQRFLIPELSNHAE 68  
 Best Local Similarity 33.2%; Score 341.5; DB 1; Length 282;  
 Matches 86; Conservative 23; Mismatches 57; Indels 13; Gaps 7;  
 Qy 24 INFSLIGATGATVQSYNTNFIRAVRGRLLTGADVRHEIPVLPN-RVGLPINQRFLIPELSNHAE 80

Db 69 LSVTALDVTVAYVGVBRAGNAYFFHDNOEAEATHLFDVQNYTFAGGGNDRL 128  
 Db 81 ESYTVALDVVNVVVAVTRAGNTAYFL--ADASTEANNVLFAGI--NEVRLPGGNDGLE 136

Qy 129 QLAGNL-RENIELGNGLPYLEAISALYYYSTGTQPLTARSLFPLICQIMISEARFOYIE 186  
 Db 137 TAAGRISRENIELGFSESETSAIGNMFRENP-GTSVP--RAFIIVIQVSEARFKYIE 191

RESULT 7  
 RIPS\_TRIKI  
 ID RIPS\_TRIKI STANDARD; PRT; 289 AA.  
 AC P24478;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein Karasurin precursor (tRNA  
 DE N-glycosidase) (EC 3.2.2.22).  
 OS Trichosanthes kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;  
 OC euroids I; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 OX NCBI\_TaxID=3677;  
 RN [1] SEQUENCE FROM N.A.  
 RC TISSUE-Root tuber; PubMed=9212998;  
 RX MEDLINE=97355562; PubMed=9212998;  
 RA Mizukami H., Lida K., Kondo T., Ogihara Y.;  
 RT "Cloning and bacterial expression of a gene encoding ribosome-  
 inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes  
 kirilowii var. japonica.";  
 RT Biol. Pharm. Bull. 20:711-713 (1997).  
 RN [2] SEQUENCE OF 24-270.  
 RP MEDLINE=2200521; PubMed=1914000;  
 RA Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;  
 RT "The complete amino acid sequence of an abortifacient protein,  
 RT karasurin.>";  
 RL Chem. Pharm. Bull. 39:1244-1249 (1991).  
 CC -!- FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC  
 CC 60S RIBOSOMAL SUBUNITS.  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenine on the 28S rRNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.

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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to license@isb-sib.ch).

CC CC EMBL; AB000666; BAA21786-1; -  
 CC DR EMBL; AB000666; BAA21786-1;  
 DR PIR; JC5606;  
 DR PIR; JU0393;  
 DR HSSP; P09389; 1MRJ;  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PRO0396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA RICIN; 1.  
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KW Toxin; Signal. 1 21 POTENTIAL.  
 FT SIGNAL 1 21 KARASURIN-A.  
 FT CHAIN 22 270 KARASURIN-A.  
 FT CHAIN 24 270 REMOVED IN MATURE FORM.  
 FT PROPEP 271 289 BY SIMILARITY.  
 FT ACT SITE 183 183 ACT SITE  
 SQ SEQUENCE 289 AA; 31704 MW; 883D3E3242887B26 CRC64;  
 Query Match 74; Conservative 74; Similarity 40.0%; Score 338; DB 1;  
 Matches 46; Mismatches 53; Indels 12; Gaps 5;  
 Qy 10 INFTTAGATVQSYNTNFIRAVRGRLLTGADVRHEIPVLPN-RVGLPINQRFLIPELSNHAE 69  
 Db 25 VSFRSLCATSSXYGVFSNLNSRKLAPYERKL-YDIPILLI--RESTLGPSQRVALHLHMYADE 81  
 Qy 70 SVTLALDVTVAYVGVBRAGNAYFFHDQDQEDA-EAITHLETFDQVRYTFAGGGNDRL 128  
 Db 82 TISVALIDTVNVYVMGTRGDTSYFF---NEASATEAKYVFDAEKVTLYSGNTVRLQ 138  
 Qy 129 QLAGNLRENIELGNGLPDEAISALYYYSTGTQPLTARSLFPLICQIMISEARFOYIE 188  
 Db 139 IAQKIRENIPILGPALDASATTLYFNMN----SAAASALMVLIISTSEARFYKEFQQ 193  
 Qy 189 MRTRI 193  
 Db 194 IGKRV 198  
 RESULT 8  
 NGKB\_SAMNI STANDARD; PRT; 563 AA.  
 ID NGKB\_SAMNI STANDARD;  
 AC P33183; P33184; B93542;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Nigrin b precursor (Rel. 41, Last annotation update)  
 DE tRNA N-glycosidase (EC 3.2.2.22); Nigrin b A chain.  
 DS Nigrin b (Contain: Nigrin V)  
 OC Sambucus nigra (European elder).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;  
 OC Asteridae; campanulids; Dipsacales; Rosaceae;  
 OC NCBI\_TaxID=4202;  
 RN [1] SEQUENCE FROM N. A.  
 RP TISSUE-Bark;  
 RC MEDLINE=96215449; PubMed=8647092;  
 RX Van Damme B.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;  
 RA Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R.,  
 RA Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;  
 RT "Characterization and molecular cloning of *Sambucus nigra* agglutinin V  
 RT (nigrin b), a GaNAc-specific type-2 ribosome-inactivating protein  
 RT from the bark of elderberry (*Sambucus nigra*).";  
 RT Eur. J. Biochem. 237:505-513 (1996).  
 RL [2] SEQUENCE OF 26-49 AND 298-321.  
 RP TISSUE-Bark;  
 RC MEDLINE=24003077; PubMed=8400135;  
 RX Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R.,  
 RA Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;  
 RT "Isolation and partial characterization of nigrin b, a non-toxic  
 RT novel type 2 ribosome-inactivating protein from the bark of Sambucus  
 RT nigra L.;"  
 RL Plant Mol. Biol. 22:1181-1186 (1993).  
 CC -!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN

PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE B-CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.  
 CC -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS  
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-  
 CC -!- INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.

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CC DR EMBL; U41299; AAB3945.1; --.  
 CC DR PIR; S37382; S37382; --.  
 CC DR InterPro; IPR0000772; Ricin\_B\_lectin.  
 CC DR InterPro; IPR001574; RIP.  
 CC DR PFam; PF00632; Ricin\_B\_lectin; 6.  
 CC DR PFam; PF00161; RIP; 1.  
 CC DR PRINTS; PR00196; SHIGARICIN.  
 CC DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 CC DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 CC DR Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; KW Glycoprotein; Lectin; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 297  
 FT CHAIN 298 563  
 FT DOMAIN 305 431  
 FT DOMAIN 434 559  
 FT DOMAIN 316 356  
 FT REPEAT 357 397  
 FT REPEAT 400 432  
 FT REPEAT 445 482  
 FT REPEAT 486 524  
 FT REPEAT 527 554  
 FT ACT SITE 188 188  
 FT DISULFID 274 302  
 FT DISULFID 319 338  
 FT DISULFID 360 377  
 FT DISULFID 448 463  
 FT DISULFID 489 506  
 FT CARBOHYD 221 221  
 FT CARBOHYD 368 368  
 FT CARBOHYD 376 376  
 FT CARBOHYD 483 483  
 FT CARBOHYD 537 537  
 FT CONFLICT 39 39  
 SQ SEQUENCE 563 AA; 62300 MW; F250CBP24621BF14 CRC64;

Query Match 32.1%; Score 330.5; DB 1; Length 563;  
 Best Local Similarity 39.5%; Pred. No. 3.7e-23; Indels 15; Gaps 4;  
 Matches 75; Conservative 39; Mismatches 61;

Qy 7 YPIINFTTAATVQSYTNFRAVGRGLTCADVRHEIPVLPNQRLFLVSNH 66  
 Db 28 YPSVTFNLQGSAATYRDFLSNRKTVATTYEQVQLRRESEVQVKSRFLVPLNTY 87  
 Qy 67 AELSVTLLADKVTNAATVQGVAGNSAYFFHDNQDAEAT-THLFDVQRYTAFGENY 124  
 Db 88 NGNTVLAIVDTNLXVVAFFGNANSYFF---KATEVQKSNLFGTQN-TISFTGNY 141  
 Qy 125 DRLEQLAGNLRNIEIENGPLEAISALYYTSTGGTQLPTLARSFLICIQMISEAARFOY 184

Db 1442 DNLETAANTRRESTELGPSPLDGAITSLYHGD-----SVARSLVVVQMYSEAARRY 194  
 Qy 185 TEGMTRTR 194  
 Db 195 IEQEVRSLQ 204

RESULT 9  
 ABRA\_ABRR STANDARD; PRT; 528 AA.  
 ID ABRA\_ABRR STANDARD; PRT; 528 AA.  
 AC P1140; P28589;  
 DT 01-JUN-1989 (Rel. 11, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DB Abrin-precursor [Contains: Abrin-a A chain (rRNA N-glycosidase); DE (EC 3.2.2.22); Abrin-a B chain].  
 OS Abrus precatorius (Indian licorice) (Crab's eye).  
 OC Eukaryote; Viriplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.  
 NCBI\_TaxID:3816; OX OR  
 RN [1] SEQUENCE FROM N.A.  
 RP RX MEDLINE=93132798; PubMed=8421313;  
 RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;  
 RT "Primary structure of three distinct isoabrinins determined by cDNA sequencing: Conservation and significance.";  
 RL J. Mol. Biol. 229:263-267(1993).  
 RN [2] SEQUENCE OF 1-251.  
 RP TISSUE=Seed;  
 RA Funatsu G., Taguchi Y., Kamenosono M., Yanaka M.;  
 RT "The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from the seeds of Abrus precatorius.";  
 RL Agric. Biol. Chem. 52:1095-1097(1988).  
 RN [3] SEQUENCE OF 1-251 FROM N.A.  
 RP TISSUE=Leaf;  
 RX MEDLINE=912011321; PubMed=2016300;  
 RA Evensen G., Mathiesen A., Sundan A.;  
 RT "Direct molecular cloning and expression of two distinct abrin A-chains".  
 RL J. Biol. Chem. 266:6848-6852(1991).  
 RN [4] SEQUENCE OF 262-528.  
 RP MEDLINE=92371656; PubMed=1505674;  
 RA Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.;  
 RT "The complete primary structure of abrin-a B chain.";  
 RL FEBS Lett. 309:115-118(1992).  
 RN X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).  
 RX MEDLINE=95333189; PubMed=1608880;  
 RA Tahirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;  
 RT "Crystal structure of abrin-a B chain".  
 RL J. Mol. Biol. 250:354-367(1995).  
 CC -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.  
 CC -!- ABRI-A IS MORE TOXIC THAN RICIN.  
 CC -!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one CC SPECIFIC ADENOSINE ON THE 28S rRNA.  
 CC -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
 CC -!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-  
 CC -!- INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.  
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DR EMBL; M98344; AAA32634\_1; ALT INIT.  
 DR EMBL; X54872; ; NOT\_ANNOTATED\_CDS.  
 DR EMBL; S32422; TZLUSA.  
 DR PDB; 1ABR; 07-PEB-95.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00052; Ricin\_B\_lectin; 6.  
 DR Pfam; PF00461; RIP; 1.  
 DR SMART; SM00458; RICIN; 2.  
 DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 DR PROSITE; PS50275; SHIGA\_RICIN; 1.  
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 KW Glycoprotein; Lectin; 3D-structure; Pyrrilidone carboxylic acid.  
 FT CHAIN 1 251 ARBIN-A CHAIN.  
 FT BEPTIDE 252 261 LINKER PEPTIDE.  
 FT CHAIN 262 528 ARBIN-A B CHAIN.  
 FT DOMAIN 400 400 RICIN B-TYPE LECTIN 1.  
 FT DOMAIN 403 527 RICIN B-TYPE LECTIN 2.  
 FT REPEAT 283 325 1 ALPHA.  
 FT REPEAT 326 366 1-BETA.  
 FT REPEAT 369 401 1-GAMMA.  
 FT REPEAT 414 449 2-ALPHA.  
 FT REPEAT 453 492 2-BETA.  
 FT REPEAT 495 528 2-GAMMA.  
 FT ACT SITE 164 164 BY SIMILARITY.  
 FT DISULFID 247 269 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 286 305 BY SIMILARITY.  
 FT DISULFID 329 346 BY SIMILARITY.  
 FT DISULFID 417 430 BY SIMILARITY.  
 FT DISULFID 456 473 BY SIMILARITY.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT CARBOHYD 361 361 N-LINKED (GLCNAC. . ).  
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . ).  
 FT CONFLICT 202 202 MISSING (IN REF. 2).  
 FT CONFLICT 298 298 N -> Y (IN REF. 4).  
 FT CONFLICT 427 427 M -> L (IN REF. 4).  
 FT CONFLICT 467 467 T -> P (IN REF. 4).  
 FT CONFLICT 483 483 V -> I (IN REF. 4).  
 FT STRAND 5 8  
 FT TURN 10 11  
 FT HELIX 14 28  
 FT STRAND 32 33  
 FT TURN 34 35  
 FT SPRAND 36 38  
 FT TURN 42 43  
 FT HELIX 47 49  
 FT STRAND 51 57  
 FT STRAND 63 69  
 FT TURN 70 72  
 FT SPRAND 75 79  
 FT STRAND 83 86  
 FT TURN 88 89  
 FT STRAND 92 93  
 FT HELIX 94 97  
 FT TURN 100 101  
 FT STRAND 103 106  
 FT TURN 113 114  
 FT HELIX 115 119  
 FT TURN 124 126  
 FT STRAND 129 129  
 FT TURN 131 142  
 FT TURN 143 144  
 FT HELIX 148 167  
 FT STRAND 168 168  
 FT HELIX 169 180  
 FT TURN 181 182

FT STRAND 185 186  
 FT HELIX 189 196  
 FT TURN 197 197  
 FT HELIX 198 207  
 FT STRAND 212 220  
 FT TURN 222 223  
 FT STRAND 226 231  
 FT TURN 232 233  
 FT HELIX 235 239  
 FT STRAND 240 240  
 FT STRAND 243 243  
 FT HELIX 290 292  
 FT TURN 296 297  
 FT STRAND 299 303  
 FT HELIX 311 313  
 FT STRAND 315 317  
 FT TURN 319 320  
 FT STRAND 322 325  
 FT TURN 326 327  
 FT STRAND 328 332  
 FT TURN 337 338  
 FT STRAND 340 344  
 FT TURN 346 348  
 FT HELIX 351 353  
 FT STRAND 355 355  
 FT STRAND 357 358  
 FT TURN 360 361  
 FT STRAND 364 366  
 FT TURN 367 370  
 FT STRAND 371 374  
 FT TURN 380 381  
 FT STRAND 383 383  
 FT STRAND 385 387  
 FT HELIX 393 395  
 FT STRAND 398 399  
 FT STRAND 406 408  
 FT STRAND 410 411  
 FT HELIX 413 415  
 FT STRAND 417 421  
 FT TURN 422 423  
 FT STRAND 424 428  
 FT TURN 432 433  
 FT HELIX 435 437  
 FT STRAND 441 444  
 FT TURN 443 444  
 FT STRAND 447 449  
 FT TURN 450 451  
 FT STRAND 452 459  
 FT TURN 464 465  
 FT STRAND 467 472  
 FT TURN 474 475  
 FT HELIX 478 480  
 FT STRAND 483 484  
 FT TURN 486 487  
 FT STRAND 490 492  
 FT TURN 493 496  
 FT STRAND 497 501

Query Match 32.0% Score 329.5 ; DB 1; Length 528;  
 Best Local Similarity 42.8% Prod. No. 4.2e-2; Mismatches 66; Indels 13; Gaps 5;

Matches 80; Conservative 28; Misconservative 10; Insertions 11; Deletions 11; Gaps 5;

QY 10 INFITAGATVQSYTNFIRAVGRGLTTPDVRHPIVLNQFILVLSNHTEL 69  
 Db 5 IKPSTEGGATISQSYKQFIALEPRLERURGG-LIHDIPVLEDPTIQLERNRYITVELNSNTE 62

QY 70 SVTLALDDVTNAYVGYRAGNSAYFFH-PDNQFDAEAITHLFTDVQNRYYTFAFGGNYDRL 127

Db 63 SIEVGIDVNTAAYVAYRAGTQSYTLRDAASSASD-----YLFGT-DHSLPFYGRYCDL 116  
 QY 128 EQLAGNLRENIELNGNPLBEAISALYYSTGGTQLPTLARSFTICIONWSEAAFRQYEG 187  
 Db 117 ERWAHQSRQOQPLGQALTHGIS--FFRSQGNDNEEKARTLIVIQVAAEAAFRYTSN 173  
 Qy 188 EMTRIR 194  
 Db 174 RVRVISIQ 180

RESULT 1.0  
 RIPI\_BRYDI STANDARD; PRT; 290 AA.

AC P33185; Q9S819;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein bryodin I precursor (tRNA N-glycosidase)  
 DE (BC 3.2-2.22) (BDI).  
 OS Bryonia dioica (Red bryony).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;  
 OC eurosidae I; Cucurbitales; Cucurbitaceae; Bryonia.  
 OX NCBI\_TaxId=3652;

RN [1] SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RP TISSUE=Leaf;  
 RX MEDLINE=97228081; PubMed=9115985;  
 RA Gawlik S.L., Neubauer M., Kies H.E., Einspahr H.M.,  
 RA Siegall C.B.;  
 RT "Molecular, biological, and preliminary structural analysis of  
 recombinant bryodin 1, a ribosome-inactivating protein from the plant  
 Bryonia dioica";  
 RT Biochemistry 36:3095-3103 (1997).  
 RN [12] RP SEQUENCE FROM N.A.  
 RA Siegall C.B.;  
 RT "Cloning and expression of a gene encoding bryodin 1 from Bryonia  
 dioica";  
 RT Patent number US5541110, 30-JUL-1996.  
 RN [3] RP SEQUENCE OF 24-66.  
 RC TISSUE=Seed;  
 RX MEDLINE=89226691; PubMed=2753586;  
 RA Montecuccini P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,  
 RA Lappi D.;  
 RT N-terminal sequence of some ribosome-inactivating proteins.";  
 RL Int. J. Pept. Protein Res. 33:263-267(1989).  
 RN [4] RP SEQUENCE OF 24-43.  
 RC TISSUE=Root;  
 RX MEDLINE=95121812; PubMed=7849072;  
 RA Siegall C.B., Gavlak S.L., Chace D., Wolff E.A., Mixan B.,  
 RA Marquardt H.;  
 RT "Characterization of ribosome-inactivating proteins isolated from  
 Bryonia dioica and their utility as carcinoma-reactive  
 immunooncogenes.;"  
 RT Bioconjug. Chem. 5:423-429(1994).  
 CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS  
 CC PROTEIN SYNTHESIS IN ANIMAL CELLS.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO  
 CC PRODUCE A SHORTER PROTEIN.  
 CC -1- BIOTECHNOLOGY: Especially useful as immunotoxin for  
 CC pharmacological applications as it has low toxicity in rats and  
 CC mice but is potent once inside target cells.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.

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 or send an email to license@isb-sib.ch).

CC EMBL; 124020; ; NOT\_ANNOTATED\_CDS.  
 DR PIR; S16491; S16491.  
 DR PDB; 1BRY; 04-MAR-98.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 DR KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal.

KW KW 23 RIBOSOME-INACTIVATING PROTEIN BRYODIN I.  
 FT SIGNAL 1 MISSING IN MATURE PROTEIN.  
 FT CHAIN 24 BY SIMILARITY.  
 FT PROPEP 270  
 FT ACT SITE 183  
 FT ACT SITE 212  
 FT CARBOHYD 214 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 214 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT MUTAGEN 250 E-XK: REDUCES ACTIVITY 10-FOLD.  
 FT CONFLICT 61 RSSIS -> LRHXI (IN REF. 3).  
 FT STRAND 25 RSSIS -> LRHXI (IN REF. 3).  
 FT TURN 30 28  
 FT TURN 31 28  
 FT HELIX 34 46  
 FT TURN 47 47  
 FT STRAND 50 54  
 FT TURN 55 56  
 FT STRAND 57 60  
 FT HELIX 66 69  
 FT STRAND 70 76  
 FT TURN 78 79  
 FT STRAND 82 88  
 FT TURN 89 92  
 FT STRAND 93 99  
 FT TURN 100 101  
 FT STRAND 102 105  
 FT HELIX 109 114  
 FT TURN 115 117  
 FT TURN 120 121  
 FT STRAND 124 127  
 FT HELIX 134 141  
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 FT HELIX 167 186  
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 FT HELIX 215 225  
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 FT STRAND 231 239  
 FT TURN 241 242  
 FT STRAND 245 250  
 FT HELIX 251 252  
 FT HELIX 254 257  
 FT TURN 258 259  
 FT STRAND 260 260  
 FT STRAND 263 263  
 FT HELIX 266 268  
 SQ SEQUENCE 290 AA; 31788 MW; E966CD9C031A42DB CRC64;

Query Match 30.3% Score 312; DB 1; Length 290;  
 Best Local Similarity 37.3%; Pred. No. 8.5e-22;  
 Matches 69; Conservative 46; Mismatches 58; Indels 12; Gaps 5;

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MIA_VISAL	STANDARD;	PRT;	254 AA.
MD_MLA_VISAL	SEQUENCE;		
RP	STRAIN=Subsp.; album;		
RC	LINEID=9715801; PubMed=8980141;		
RX	Solier M.H., Stoeva S., Schwamborn C., Wilhelm S., Stiefel T.,		
RA	Voelter W.,		
RL	"Complete amino acid sequence of the A chain of mistletoe lectin I.";		
FEBS Lett. 339:153-157(1996).			
RT	-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4, 324 OF 28 S rRNA. THE B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY INTO THE CELL OF THE A CHAIN. B CHAINS ARE ALSO RESPONSIBLE FOR CELL AGGLOMERATION (LECTIN ACTIVITY).		
CC	-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.		
CC	-!- SUBUNIT: Disulfide-linked dimer of A and B chains.		
CC	-!- PHARMACEUTICAL: Due to its immunomodulatory effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid tumors.		
CC	-!- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA AND NON-GLYCOSYLATED FORM MLA.		
CC	-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.		
CC	TYPE 2 RIP SUBFAMILY.		
PIR; PD00118; PD0018			
DR	HSSP; P11140; LABR.		
DR	InterPro; IPR001574; RIP.		
DR	PFam; PF00161; RIP; 1.		
DR	PROSITE; PS000275; SHIGA_RICIN.		
KW	Plant defense; Hydrolase; Toxin; Repeat; Glycoprotein; Lectin.		
FT	ACT SITE 165 165 N-LINKED (GHCNAC. . .).		
FT	CARBHYD 112 112 N-LINKED (MLA').		
FT	VARIANT 15 15 V > D (IN MLA').		
FT	VARIANT 66 66 Y > I (IN MLA').		
FT	VARIANT 112 112 N > T (IN MLA').		
FT	VARIANT 116 116 P > T (IN MLA').		
FT	VARIANT 133 134 DQ -> BE (IN MLA').		
FT	VARIANT 140 140 T > S (IN MLA').		
FT	VARIANT 144 144 F > Y (IN MLA').		
FT	VARIANT 151 151 T > A (IN MLA').		
FT	VARIANT 179 179 Y > D (IN MLA').		
FT	VARIANT 184 184 A > E (IN MLA').		
FT	VARIANT 190 190 V > M (IN MLA').		
FT	VARIANT 218 218 I > P (IN MLA').		
FT	VARIANT 223 224 PP -> ST (IN MLA').		
FT	VARIANT 231 231 T > S (IN MLA').		
FT	VARIANT 235 235 D > S (IN MLA').		
SEQUENCE;	28478 MW;	53BAF8D3OFFEE67 CRC64;	
Qy	Query Match Score 284.5; Best Local Similarity 33.5%; Pred. No. 2.9e-19; Matches 63; Conservative 45; Mismatches 69; Indels 11; Gaps 3;		
Db	2 VRFSLGSSTSSTSYSKPFGKSTVILPVGNYLTKLQT 135		
Qy	14 TAGATVQSYTNTVYGRNLTTGADVREHEIPVLPNVLGPIN-QRFILVELNHAELSV 71		
Db	9 THOTTGEYEFRTFLRDYSSS-FSNEIPLL-RQSTIPVSDAQRFVLLTNGQDSV 66		
Qy	70 SYTIALDVTNAVYVGRAGNSAYFFPHDNOEADAEATHLFLTDVQNRRTFAFGGNYDQEKGK 78		
Db	72 TAIDVNTMAYVGYAGNSAYFFPHDNOEADAEATHLFLTDVQNRRTFAFGGNYDQEKGK 135		

Qy 130 LAGNLRENIELNGPLEBAISLYYYSTGGTQLPTLARSFFICIQMISEAARFOYIEGEM 189  
 Db 136 AAGKIREKIPPLGFPAUDSAITLFLHYDS---TAAAAFLVTTAEASRFKTYEGQI 190  
 Qy 190 RTRIRYN 197  
 Db 191 IERISKNQ 198  
 Qy 191 :  
 Db 192 :  
 RN Search completed: February 10, 2004, 16:23:26  
 Job time : 7.67161 secs

## RESULT 15

RIP2\_MOMBA  
ID RIP2\_MOMBA  
AC P29359;

DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ribosome-inactivating protein momordin II precursor (rRNA

DE N-Glycosidase) (EC 3.2.2.22)  
 OS *Momordica balsamina* (Bitter gourd) (Balsam pear).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC euroids I; Cucurbitales; Cucurbitaceae; Momordicae;

OC NCBI\_TaxID=3672;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC ISSUE-Seed/  
 RX MEDLINE=9302170; PubMed=1408771;

RA Ortigao M. Better M.;  
 RT "Momordin II, a ribosome inactivating protein from *Momordica*  
 balsamina, is homologous to other plant proteins.";

RL Nucleic Acids Res. 20:4662-4662 (1992).

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 specific adenosine on the 28S rRNA.

CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC -!- TYPE 1 RIP SUBFAMILY.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; Z12175; CAA78166.1; -.

DR PIR; S25560; S25560.

DR PDB; 1CFP; 07-JUN-99.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00336; SHIGARICIN.

DR PROSITE; PS00275; SHIGA\_RICIN; 1.

KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;

KW 3D-structure.

FT SIGNAL 1 23

FT CHAIN 24 286 RIBOSOME-INACTIVATING PROTEIN MOMORDIN

FT 181 181 II. BY SIMILARITY.

FT SEQUENCE 286 AA; 32031 MW; 3B89FF1AE6B25986 CRC64;

Query Match 27.1%; Score 279; DB 1; Length 286;  
 Best Local Similarity 35.3%; Fred. No. 9.8e-19;  
 Matches 66; Conservative 42; Mismatches 67; Indels 12; Gaps 5;

Qy 10 INFTTAGATGVSYTNTFRAVEGRLLTGADYFHEIPVLPNRGLPNQRFLVELSNHAEI 69

Db 25 VNFDSLTAATCYTKTEEDFATLPLFSHKV-YDIPLYSTS--DSRRFLFDLTSAYE 81

Qy 70 SYTLAIDVTNVYVGGRAGNSAYFFFHDNQDDEAITHLFTDVQNRYFAFGNYDRLEQ 129

Db 82 TISVAIDVTNVYVAVRTRDSYFF--KESSPEAVNILFKGTR-KITLPYGTNYENLQT 137

Qy 130 LAGNLRENIELNGPLEBAISLYYYSTGGTQLPTLARSFFICIQMISEAARFOYIEGEM 189

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:00 ; Search time 26.6864 Seconds  
 (without alignments)  
 1933.961 Million cell updates/sec

Title: US-10-083-336A-10  
 Perfect score: 1029  
 Sequence: 1 MIFPKQYPLINFTTAGATVQ.....RFQYIEGEMRTRIYNRSA 200

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs., 258052604 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

SPTRMBL23:  
 Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mic:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodont:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriopl:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1021	99.2	541	10	Q41174	Q41174 ricinus com
2	401.5	39.0	580	10	Q94BW4	Q94bw3 cinnamomum
3	397.5	38.6	580	10	Q94BW4	Q94bw4 cinnamomum
4	397.5	38.6	581	10	Q94BW5	Q94bw5 cinnamomum
5	395.5	38.4	549	10	Q9FV22	Q9Fv22 cinnamomum
6	350.5	34.1	563	10	Q04367	Q04367 sambucus ni
7	347.5	33.8	564	10	Q9AVR2	Q9avr2 sambucus eb
8	344.5	33.5	528	10	Q06076	Q06076 abrus preca
9	340.5	33.0	289	10	Q94KE4	Q9ake4 trichosanth
10	338	32.8	247	10	Q9LRE3	Q9lre3 trichosanth
11	338	32.8	289	10	Q41216	Q41216 trichosanth
12	336.5	32.7	252	10	Q38760	Q38760 abrus preca
13	330.5	32.1	563	10	Q94GS2	Q94gs2 sambucus ni
14	330.5	32.1	563	10	Q8GT32	Q8gt32 sambucus ni
15	329.5	32.0	252	10	Q38761	Q38761 abrus preca
16	324.5	31.5	270	10	Q8LPV7	Q8lpv7 trichosanth

17	323.5	31.4	251	10	Q96236	Q96236 abrus preca
18	322.5	31.3	251	10	Q96237	Q96237 abrus preca
19	319	31.0	565	10	Q04071	Q04071 sambucus ni
20	317	30.8	270	10	Q41611	Q41611 trichosanth
21	316.5	30.8	251	10	Q96235	Q96235 abrus preca
22	314.5	30.6	547	10	Q9M6E9	Q9m6e9 abrus preca
23	310.5	30.2	566	10	Q04072	Q04072 sambucus ni
24	307.5	29.9	278	10	Q00980	Q00980 luffa cylindrica
25	291	28.3	570	10	Q41358	Q41358 sambucus ni
26	285	27.7	249	10	Q8LKQ5	Q8lkq5 viscum album
27	285	27.6	570	10	Q22415	Q22415 sambucus ni
28	283	27.5	251	10	Q8LKQ4	Q8lkq4 viscum album
29	283	27.4	254	10	Q8LKQ6	Q8lkq6 momordica charantia
30	280	27.2	264	10	Q9FSH2	Q9fsh2 momordica charantia
31	280	27.2	264	10	Q8S452	Q8s452 jatropha curcas
32	278	27.0	293	10	Q8W243	Q8w243 viscum album
33	277.5	27.0	565	10	Q9FUV7	Q9fv7 momordica charantia
34	277	26.9	286	10	P93543	P93543 sambucus nigra
35	277	26.9	569	10	P94356	P94356 polygonatum multiflorum
36	275	26.7	531	10	Q8RXH6	Q8rxh6 viscum album
37	273	26.5	249	10	Q8RXH7	Q8rxh7 viscum album
38	272	26.4	286	10	Q41257	Q41257 momordica charantia
39	272	26.4	298	10	Q04358	Q04358 iris holanensis
40	270	26.2	592	10	Q8W2E7	Q8w2e7 iris holanensis
41	268	26.0	300	10	Q9M653	Q9m653 polygonatum multiflorum
42	266.5	25.9	603	10	Q8GZN9	Q8gzn9 euphorbia strictifolia
43	262.5	25.5	299	10	Q8VYU0	Q8vyu0 jatropha curcas
44	261	25.4	293	10	Q8W2E8	Q8w2e8 iris holanensis

## ALIGNMENTS

RESULT 1				
041174	ID	Q41174	PRELIMINARY;	
041174	AC	Q41174	PRT;	541 AA.
01-NOV-1996	(TRMBLrel)	01	Last sequence update)	
01-NOV-1996	(TRMBLrel)	01	Last sequence update)	
01-MAR-2003	(TRMBLrel)	23	Last annotation update)	
DE	Protein A chain (EC 3.2.2.22) (rRNA N-glycosidase)			
DE	(Fragment).			
OS	Ricinus communis (Castor bean).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Rosidae; OC			
CC	eurosid I; Malpighiales; Euphorbiaceae; Ricinus. NCBI_TaxID=3988;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	REIDLINE: 92333377; PubMed:1633311;			
RA	Robert L.M.; Tregear J.W.; Lord J.M.; Robert L.M.; Tregear J.W.; Lord J.M.; "Molecular Cloning of ricin."			
RR	Targeted Diagn. Ther. 7:81-97 (1992).			
RC	"CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE POSITION ON THE 28S RRNA.			
CC	"SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.			
CD	EMBL: SA0366; AA02582.1; --.			
DR	HSSP; P02879; 1BR6.			
DR	InterPro; IPR000772; Ricin_B_lectin.			
DR	InterPro; IPR000574; RIP.			
DR	InterPro; IPR001400; Somatotropin.			
DR	InterPro; IPR00652; Ricin_B_lectin; 6.			
DR	Pfam; PF00161; RIP; 1.			
DR	PRINTS; PR00396; SHIGARICIN.			
DR	SMART; SM00458; RICIN; 2.			
DR	PROSITE; PS50231; RICIN_B_LECTIN.			
DR	PROSITE; PS00275; SHIGA_RICIN; 1.			
DR	PROSITE; PS03338; SOMATOTROPIN_2; 1.			
KW	Hydrolase; Toxin.			
FT	NON_TER			
SEQUENCE	541 AA;	1		
SQ	60281 MW;	2B7B2CDEF1F2E9D9 CRC64;		

Result No.	Score	Query	Match	Length	DB ID	Description
1	1021	99.2	541	10	Q41174	Q41174 ricinus communis
2	401.5	39.0	580	10	Q94BW4	Q94bw3 cinnamomum
3	397.5	38.6	580	10	Q94BW4	Q94bw4 cinnamomum
4	397.5	38.6	581	10	Q94BW5	Q94bw5 cinnamomum
5	395.5	38.4	549	10	Q9FV22	Q9fv22 cinnamomum
6	350.5	34.1	563	10	Q04367	Q04367 sambucus nigra
7	347.5	33.8	564	10	Q9AVR2	Q9avr2 sambucus nigra
8	344.5	33.5	528	10	Q06076	Q06076 abrus precatorius
9	340.5	33.0	289	10	Q94KE4	Q9ake4 trichosanthus
10	338	32.8	247	10	Q9LRE3	Q9lre3 trichosanthus
11	338	32.8	289	10	Q41216	Q41216 trichosanthus
12	336.5	32.7	252	10	Q38760	Q38760 abrus precatorius
13	330.5	32.1	563	10	Q94GS2	Q94gs2 sambucus nigra
14	330.5	32.1	563	10	Q8GT32	Q8gt32 sambucus nigra
15	329.5	32.0	252	10	Q38761	Q38761 abrus precatorius
16	324.5	31.5	270	10	Q8LPV7	Q8lpv7 trichosanthus





Query Match	34.1%	Score 350.5; DB 10; Length 563;	Y	QY	125 DRLQLAGNLRENTIELGGPLEAISALYYSTGGTQPLTSLRSLFICIQMSEARFY 184
Best Local Similarity	41.6%	Pred. No. 1.9e-24; Pred. No. 1.9e-24;	Y	Db	142 DNLETAAGRRESIELGGDPLGAITSLWY--DGG---VARSLLVLIQMVEARFY 194
Matches 79; Conservative Matches 40; Mismatches 56; Indels 15; Gaps 4;					
Y	7 YPLINFTTAGATOSYTINFIRAVGRLLTGADYRHEIPVLNRVGLPINQRTFLVELSNH 66	QY	185 IEGERMRTRIR 194	Db	195 IEQEVVRSLQ 204
Y	28 YPSVSNLAGAKSATYRDPLKNLRTIVATGYEVNGLPVLRRESEVOVKNRFLVLLTN 87	Db	195 IEQEVVRSLQ 204		
Y	67 AELSYTTLAIDVTNAYVVGYRAGNSAYFFHDNQDEAEI--THLFDTQNRYTAFFGNY 124	RESULT 8			
Y	88 NGNTVTLAVITNLXVAFSANANSYFF----KDATQLSNSLFGTR-QHTLPTGNY 141	Q06076	PRELIMINARY;	PRT;	528 AA.
Y	125 DRLEOLAGNIRENTIELGGPLEEAIISALYYSTGGTQPLTSLRSLFICIQMSEARFY 184	AC Q06076;	(TREMBLER. 01, Created)		
Y	142 DNLETAAGRRESIELGGDPLGAITSLWY----SVARSLLVLIQMVEARFY 194	AC Q06076;	(TREMBLER. 01, Last sequence update)		
Y	185 IEGERMRTRIR 194	AC Q06076;	(TREMBLER. 01, Last annotation update)		
Y	195 IEQEVVRSLQ 204	AC Q06076;	(TREMBLER. 03, Last annotation update)		
Y	7 YPLINFTTAGATOSYTINFIRAVGRLLTGADYRHEIPVLNRVGLPINQRTFLVELSNH 66	DE Abra-in-d (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).			
X	28 YPSVSNLAGAKSATYRDPLKNLRTIVATGYEVNGLPVLRRESEVOVKNRFLVLLTN 87	OS Abrus precatorius (Indian licorice) (Crab's eye).			
X	67 AELSYTTLAIDVTNAYVVGYRAGNSAYFFHDNQDEAEI--THLFDTQNRYTAFFGNY 124	OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;			
X	88 NGNTVTLAVITNLXVAFSANANSYFF----KDATQLSNSLFGTR-QHTLPTGNY 141	OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
X	125 DRLEOLAGNIRENTIELGGPLEEAIISALYYSTGGTQPLTSLRSLFICIQMSEARFY 184	OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.			
X	142 DNLETAAGRRESIELGGDPLGAITSLWY----SVARSLLVLIQMVEARFY 194	NCBI_TaxID=3816; RN [1]			
X	185 IEGERMRTRIR 194	RN [1]	SEQUENCE FROM N.A.		
X	195 IEQEVVRSLQ 204	PP RX MEDLINE=3132198; PubMed=8421313;			
X	7 YPLINFTTAGATOSYTINFIRAVGRLLTGADYRHEIPVLNRVGLPINQRTFLVELSNH 66	RA Hung C.-H., Lee, M.-C., Lee, T.-C., Lin, J.-Y.;			
X	28 YPSVSNLAGAKSATYRDPLKNLRTIVATGYEVNGLPVLRRESEVOVKNRFLVLLTN 87	RT "Primary structure of three distinct isoforms determined by cDNA sequencing: conservation and significance.";			
X	67 AELSYTTLAIDVTNAYVVGYRAGNSAYFFHDNQDEAEI--THLFDTQNRYTAFFGNY 124	RT J. Mol. Biol. 229:263-267 (1993).			
X	88 NGNTVTLAVITNLXVAFSANANSYFF----KDATQLSNSLFGTR-QHTLPTGNY 141	CC -!- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE POSITION: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.			
X	125 DRLEOLAGNIRENTIELGGPLEEAIISALYYSTGGTQPLTSLRSLFICIQMSEARFY 184	CC -!- SIMILARITY: BELONGS TO THE 28S RNA.			
X	142 DNLETAAGRRESIELGGDPLGAITSLWY----SVARSLLVLIQMVEARFY 194	CC -!- SPECIFIC ADENOSINE ON THE 28S RNA.			
X	185 IEGERMRTRIR 194	CC -!- DR EMBL_M98346; AAA32626.1; -.			
X	195 IEQEVVRSLQ 204	DR InterPro: IPR000772; Ricin_B_lectin.			
X	7 YPLINFTTAGATOSYTINFIRAVGRLLTGADYRHEIPVLNRVGLPINQRTFLVELSNH 66	DR InterPro: IPR001574; RIP.			
X	28 YPSVSNLAGAKSATYRDPLKNLRTIVATGYEVNGLPVLRRESEVOVKNRFLVLLTN 87	DR Pfam: PF001652; Ricin_B_lectin; 6.			
X	67 AELSYTTLAIDVTNAYVVGYRAGNSAYFFHDNQDEAEI--THLFDTQNRYTAFFGNY 124	DR Pfam: PF001652; RIP; 1.			
X	88 NGNTVTLAVITNLXVAFSANANSYFF----KDATQLSNSLFGTR-QHTLPTGNY 141	DR PRIMUS; PR0036; SHIGARICIN.			
X	125 DRLEOLAGNIRENTIELGGPLEEAIISALYYSTGGTQPLTSLRSLFICIQMSEARFY 184	DR SMART; SM00458; RICIN; 2.			
X	142 DNLETAAGRRESIELGGDPLGAITSLWY----SVARSLLVLIQMVEARFY 194	DR PROSITE; PS50231; RICIN_B_LECTIN; 1.			
X	185 IEGERMRTRIR 194	DR PROSITE; PS00275; SHIGA_RICIN; 1.			
X	195 IEQEVVRSLQ 204	KW Hydrolase; Toxin.			
X	7 YPLINFTTAGATOSYTINFIRAVGRLLTGADYRHEIPVLNRVGLPINQRTFLVELSNH 66	FT NON_TER 1 1			
X	28 YPSVSNLAGAKSATYRDPLKNLRTIVATGYEVNGLPVLRRESEVOVKNRFLVLLTN 87	FT NON_TER 528 528 AA; 528870 MW; 62ED42FB9FF60F8 CRC64;			
X	67 AELSYTTLAIDVTNAYVVGYRAGNSAYFFHDNQDEAEI--THLFDTQNRYTAFFGNY 124	Query Match 33.5%; Score 344.5%; DB 10; Length 528;			
X	88 NGNTVTLAVITNLXVAFSANANSYFF----KDATQLSNSLFGTR-QHTLPTGNY 141	Best Local Similarity 45.0%; Pred. No. 6.3e-24; Indels 9; Gaps 4;			
X	125 DRLEOLAGNIRENTIELGGPLEEAIISALYYSTGGTQPLTSLRSLFICIQMSEARFY 184	Matches 85; Conservative 24; Mismatches 71; Indels 9; Gaps 4;			
X	142 DNLETAAGRRESIELGGDPLGAITSLWY----SVARSLLVLIQMVEARFY 194	QY 6 QYPINNETTAGATOSYTINFIRAVGRLLTGADYRHEIPVLNRVGLPINQRTFLVELSNH 66			
X	185 IEGERMRTRIR 194	Db 1 QDQVQKPTTGGATOSYKOFTEALQRQLTGG--LTHIDIPVLPDPDTVEERNRYTVELSN 58			
X	195 IEQEVVRSLQ 204	QY 6 HABLSVLLADLVNVAVGVFRAGNSAYFFHDNQDEAEATHLFTTQNRYTEAFGNYD 125			
X	7 YPLINFTTAGATOSYTINFIRAVGRLLTGADYRHEIPVLNRVGLPINQRTFLVELSNH 66	Db 1 QDQVQKPTTGGATOSYKOFTEALQRQLTGG--LTHIDIPVLPDPDTVEERNRYTVELSN 58			
X	28 YPSVSNLAGAKSATYRDPLKNLRTIVATGYEVNGLPVLRRESEVOVKNRFLVLLTN 87	QY 59 SERESLEVGDVNTAVVAYRAGSQSYEL--RDAASASTYLEPFTQ-RYSLRFQSGY 114			
X	67 AELSYTTLAIDVTNAYVVGYRAGNSAYFFHDNQDEAEI--THLFDTQNRYTAFFGNY 124	Db 126 RLEQLAGNLRENTIELGGPLEAISALYYSTGGTQPLTSLRSLFICIQMSEARFY 185			
X	88 NGNTVTLAVITNLXVAFSANANSYFF----KDATQLSNSLFGTR-QHTLPTGNY 141	Db 115 DIERWAHQTRBISLQLQALTHAS--FLRGSGASNDEEKARTLIVTIONMASEARFYRCI 171			
X	125 DRLEOLAGNIRENTIELGGPLEEAIISALYYSTGGTQPLTSLRSLFICIQMSEARFY 184	QY 186 IEGERMRTRIR 194			
X	142 DNLETAAGRRESIELGGDPLGAITSLWY----SVARSLLVLIQMVEARFY 194	Db 172 SNRVGJSIR 180			
X	185 IEGERMRTRIR 194	RESULT 9			
X	195 IEQEVVRSLQ 204	Q4 KE4 PRELIMINARY;	PRT;	289 AA.	
X	7 YPLINFTTAGATOSYTINFIRAVGRLLTGADYRHEIPVLNRVGLPINQRTFLVELSNH 66	ID Q4 KE4			
X	28 YPSVSNLAGAKSATYRDPLKNLRTIVATGYEVNGLPVLRRESEVOVKNRFLVLLTN 87	AC Q4 KE4			
X	67 AELSYTTLAIDVTNAYVVGYRAGNSAYFFHDNQDEAEI--THLFDTQNRYTAFFGNY 124	DB 01-DEC-2001 (TREMBLER) 19			
X	88 NGNTVTLAVITNLXVAFSANANSYFF----KDATQLSNSLFGTR-QHTLPTGNY 141				



RESULT 13		RESULT 14	
Db	177 GVSIR 181	Db	Q8GT32
	Q945S2	ID	Q8GT32
	AC Q945S2;	AC Q8GT32;	PRELIM
	DT 01-DEC-2001 (TREMBI)	DT 01-MAR-2003 (TREMBI)	
	DT 01-DEC-2001 (TREMBI)	DT 01-MAR-2003 (TREMBI)	
	DT 01-MAR-2003 (TREMBI)	DE Type 2 ribosome-ii	
	DE Ribosome-inactivating protein	DE (EC 3.2.2.22).	
	DE N-Glycosidase	DE Sambucus nigra (Eu-	
	AVL,	Bukaryota; Viridipla-	
	OS sambucus nigra	Spermatozoa; Magn-	
	OC Eukaryota; Viridipla-	Asteridae; Campanu-	
	OC Spearmatophyta	m	
	OC Asteridae; campanu-	m	
	NCBI_TaxID=4202;	OX [1]	
	RN	SEQUENCE FROM N.A.	
	RP TISSUE=Leaf;	RT Van Damme B.J.M.	
	RC	"Characterization	
	RA proteins from Sam-	RT Submitted (AUG-200	
	RA bu	-); CATALYTIC ACTI	
	RA V	ONIC ADENO	
	RA	- - SIMILARITY: BE	
	RA EMBL: AF401335; AA	EMBL: AF401335; AA	
	DR InterPro; IPR000717	DR InterPro; IPR000717	
	DR InterPro; IPR00157	DR Pfam; PF00652; Ric-	
	DR Pfam; PF00161; RIP	DR Pfam; PF00161; RIP	
	DR PRINTS; PRO0396; S	DR SMART; SM00458; RI	
	DR PROSITE; PS00231;	DR PROSITE; PS00231;	
	DR PROSITE; PS00275;	DR PROSITE; PS00275;	
	KW Hydrolase; Toxin.	KW Hydrolase; Toxin.	
	SQ SEQUENCE: 563 AA;	SQ SEQUENCE: 75; Consense	
		Query Match Best Local Similarity Matches	
Qy	7 YPLINFTTA	Qy 7 YPLINFTTA	
	:	:	
Db	28 YPSVFSNL	Db 28 NGNTVTL	
		:	
Qy	67 AELSVTLAI	Qy 125 DRLEQLAGN	
Db	88 NGNTVTL	Db 142 DNLTEATAANT	
		:	
Qy	165 IEGERMRTR	Qy 195 IEQEVRRSI	
Db			

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.  
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.  
 RN [1] NCBI\_TaxID:4202;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Leaf;  
 RA Girbes T., Arias F.J., Antolin P.;  
 RT "characterization and molecular cloning of Nigrin 1, a type two  
 ribosome-inactivating protein from leaves of elder (*Sambucus nigra*).";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF24280; AAN86130.1; -.  
 KW Hydrolase; Glycosidase;  
 SQ SEQUENCE 563 AA; 62173 MW;

Query Match 32.1%; Score 330.5; DB 10; Length 563;  
 Best Local Similarity 39.5%; Pred. No. 1 4e-22;  
 Matches 75; Conservative 39; Mismatches 61; Indels 15; Gaps 4;  
 Qy 7 YPINTINFTAGATVQSYNTNFIRAVRGRITGAVRHEPPVLPNVRGLDINQRFLVELSNH 66  
 Db 28 HESVSTNLGDGKSAHTDFLSNKRIVATGTYEVNGPVLRESEYQVKSPRLVLTNY 97  
 Qy 67 AELSYTTLADVTNAVYGYRAGNSAYFFHDNQEDAAI--THLEFLDVQNRVTEARGNY 124  
 Db 88 NGNTVLAADVNLWVAFSGNATQYEG--KDATEVQKSNLFVTKQN-TLSFGNY 141  
 Qy 125 DRLEQLAQNLRNENIQLONGPYLEASALYYSTGGTQLPTLARSFICIONMSEARFYQ 184  
 Db 142 DNLTEATAANTRRESTEELGPSPLDGATISLXHGDD-----SVARSLLVVQMVSEARFRY 194  
 Qy 185 IESEBMTRIR 194  
 Db 195 IEGEYVRSIQ 204

## RESULT 15

Q38761 ID Q38761 PRELIMINARY; PRT; 252 AA.

AC Q38761; Q96734;

DT 01-NOV-1996 (TREMBrel. 01, Created)

DT 01-OCT-2002 (TREMBrel. 22, Last annotation update)

DE Ricin A-chain type 73 (EC 3.2.2.22) (rRNA N-glycosidase)  
 DE (fragment).

RN

OS *Abrus precatorius* (Indian licorice) (Crab's eye).OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.

RN NCBI\_TaxID:3816;

RN

RP SEQUENCE FROM N.A.

RC TISSUE=Leaf;

RA Evensen G., Mathiesen A., Sundan A.;  
 RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.

RN

RP SEQUENCE OF 2-252 FROM N.A.

RC TISSUE=Seed;

RX MEDLINE=4139756; PubMed=8307038;

RA Chih-Hung H., Lee M.C., Chen J.-K., Lin J.-Y.;

RT "Cloning and expression of three abrin A-chains and their mutants  
 derived by site-specific mutagenesis in *Escherichia coli*.";

RL Eur. J. Biochem. 219:83-87(1994).

CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 SPECIFIC ADENOSTINE ON THE 28S RNA.

CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

DR EMBL; X54873; CAA38655.1; -.

DR EMBL; X76720; CAA54138.1; -.

DR HSSP; P11140; IABR.

DR InterPro; IPR01574; RIP.

DR Pfam; PF0161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA\_RICIN\_1.

KW Glycosidase; Hydrolase; Toxin.  
 FT NON\_TER 252 252  
 SQ SEQUENCE 252 AA; 187B8B4134AECE5 CRC64;  
 Query Match 32.0%; Score 329.5; DB 10; Length 252;  
 Best Local Similarity 42.8%; Pred. No. 5 8e-23;  
 Matches 80; Conservative 28; Mismatches 66; Indels 13; Gaps 5;  
 Qy 10 INFETAGATQSYNTNFIRAVRGRITGAVRHEPPVLPNVRGLDINQRFLVELSNH 69  
 Db 6 IKFSTEGATQSQYKQFIEALRERRGG-LIHDPVLPDPITLQERNRYTVELNSDTE 63  
 Qy 70 SVTLLADVTNAVYGYRAGNSAYFFF-PDNQBEDAETHLFTDVQNRVTFAGGNYDRL 127  
 Db 44 SIEVGIDVTNRYVVAAGTOSYFLRDAPSASD----YLFTGT-DQHSLPFYGYGDL 117  
 Qy 128 EQLAGNIRENTELNGPLEEAISALYYSTGTOLPTLARSFICIONMSEARFYEG 187  
 Db 118 ERWAHSQQIPLGQLALTGIS--FRRGGNDNEEKARTLIVIVQMVAEARFRYISN 174  
 Db 64 SIEVGIDVTNRYVVAAGTOSYFLRDAPSASD----YLFTGT-DQHSLPFYGYGDL 117  
 Qy 188 EMRTRTR 194  
 Db 175 RVRSVSIQ 181

Search completed: February 10, 2004, 16:26:39  
 Job time : 26.6564 secs



PT Analogues of type I ribosome inactivating protein - useful as  
 PT cytotoxic agents, immuno toxins for treating auto immune diseases,  
 PT cancer, graft versus host disease and selective cell killing in-vivo  
 XX

PS Claim 1; Page 92; 163pp; English.

CC The invention covers analogues of Type I RIPS. Ricin is a Type II  
 CC RIP whose A chain is homologous to plant type I RIPS. The analogues  
 CC of the invention have a cysteine available for intermolecular  
 CC disulphide bonding at an amino acid position corr esp. to a position  
 CC not naturally available for bonding; the cys residue is located in  
 CC the C-terminal region of the analogue between the position corr esp. to  
 CC amino acid 251 and the C-terminus of ricin A chain. The analogues are  
 CC pref. joined via a disulphide linkage to a molecule which specifically  
 CC binds to a target cell, e.g. an antibody fragment.  
 CC (Updated on 09-JAN-2003 to add missing OS field.)  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 267 AA;

Query Match 97.9%; Score 955; DB 14; Length 267;  
 Best Local Similarity 95.0%; Pred. No. 3.-e-94;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;  
 Qy 2 IFPKQYPLINFTAGATVQSYTNFIRAVRGRLT-----VLPNRYGLPINQRFILV 51  
 Db 1 IFPKQYPLINFTAGATVQSYTNFIRAVRGRLT-----VLPNRYGLPINQRFILV 60  
 Qy 52 ELSNHAEVLSTLADVNAYVGYRAGNSAYFHPDQNEDAATHLFTDVQNRYTFAG 111  
 Db 61 ELSNHAEVLSTLADVNAYVGYRAGNSAYFHPDQNEDAATHLFTDVQNRYTFAG 120  
 Qy 112 GNYDRLEQLAGNLRENIELGNGPLEAISALYYSTGGTOLPLTLARSFIICIQMISEAAR 171  
 Db 121 GNYDRLEQLAGNLRENIELGNGPLEAISALYYSTGGTOLPLTLARSFIICIQMISEAAR 180  
 Qy 172 FOYIEGEMTRIRYNRSA 190  
 Db 181 FOYIEGEMTRIRYNRSA 199

RESULT 2  
 AAR63902 standard; protein; 267 AA.  
 ID AAR63902  
 XX AC AAR63902;  
 DT 25-MAR-2003 (updated)  
 DT 27-JUL-1995 (first entry)  
 XX DE Ricin A-chain (RTA).  
 XX Ricin A chain; RTA; ribosome-inactivating proteins; RIPS;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.  
 OS Ricinus communis.  
 XX WO9426910-A1.  
 PN 24-NOV-1994.  
 PD 12-MAY-1994; 94WO-US05348.  
 XX PR 12-MAY-1993; 93US-0064691.  
 XX PA (XOMA ) XOMA CORP.  
 XX Better MD, Carroll SS, Studnicka GM, Carroll SF;  
 PR Better MD, Carroll SS, Studnicka GM, Carroll SF;  
 XX DR WPI; 1995-006804/01.  
 XX PT Polynucleotide(s) encoding type I ribosome-inactivating proteins

- which are suitable for use as components of cytotoxic therapeutic agents.

XX Example 3; Fig 1; 221pp; English.

CC AAR63902 is the ricin A chain gene product, it is analogous to the  
 CC ribosome-inactivating proteins (RIPs) described in AAR63903-R63911.  
 CC RIPs are the key components of cytotoxic therapeutic agents (CTAs),  
 CC which include gene fusion products and immunoconjugates. CTAs may  
 CC be used to selectively eliminate any cell type to which a RIP  
 CC component is targeted, by the specific binding capacity of the  
 CC second component of the agent. They can be used in the treatment  
 CC of diseases where the elimination of a particular cell type is  
 CC desired, such as autoimmune disease, cancer and graft-versus-host  
 CC disease.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 267 AA;

Query Match 97.9%; Score 955; DB 16; Length 267;  
 Best Local Similarity 95.0%; Pred. No. 3.7-e-94;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;  
 Qy 2 IFPKQYPLINFTAGATVQSYTNFIRAVRGRLT-----VLPNRYGLPINQRFILV 51  
 Db 1 IFPKQYPLINFTAGATVQSYTNFIRAVRGRLT-----VLPNRYGLPINQRFILV 60  
 Qy 52 ELSNHAEVLSTLADVNAYVGYRAGNSAYFHPDQNEDAATHLFTDVQNRYTFAG 111  
 Db 61 ELSNHAEVLSTLADVNAYVGYRAGNSAYFHPDQNEDAATHLFTDVQNRYTFAG 120  
 Qy 112 GNYDRLEQLAGNLRENIELGNGPLEAISALYYSTGGTOLPLTLARSFIICIQMISEAAR 171  
 Db 121 GNYDRLEQLAGNLRENIELGNGPLEAISALYYSTGGTOLPLTLARSFIICIQMISEAAR 180  
 Qy 172 FOYIEGEMTRIRYNRSA 190  
 Db 181 FOYIEGEMTRIRYNRSA 199

RESULT 3

AAW25136 standard; protein; 290 AA.  
 ID AAW25136  
 XX AC AAW25136;  
 XX DT 25-MAR-2003 (updated)  
 DT 02-DEC-1997 (first entry)  
 XX DE Ricin A-chain ribosome inhibitory protein inactive precursor.  
 XX Maize; ProRIP; ribosome inactivating protein; alpha; beta subunit;  
 KW internal linker; Barley Translation Inhibitor; Trichosanthin;  
 KW Ricin A-chain; Abrin A; Abchin; Saporin; SIT-1; Luffin A; MAP;  
 KW Ricinus communis agglutinin; Momordin; Pap-S; Luffin-B; Dianthin 30;  
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;  
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome.  
 XX OS Synthetic.  
 XX PN US5646026-A.  
 XX PD 08-JUL-1997.  
 XX PR 07-JUN-1995; 95US-0485286.  
 XX PR 09-DEC-1992; 92US-0987927.  
 PR 11-JUN-1990; 90US-0535636.  
 PR 26-JAN-1995; 95US-0378761.  
 PR 07-JUN-1995; 95US-0485286.  
 XX PA (DOWC ) DOWELANCO.

/note= "Position of possible insertion of internal peptide linker sequence"

<p>PT PT LX Hey TD, Morgan AER, Walsh TA; I1 WPI: 1997-362934/33.</p> <p>CX DNA encoding pro-ribosome inactivating proteins - inactive PT precursors of ribosome inactivating proteins; can be expressed in eukaryotic cells without causing cell death</p> <p>CX Claim 4; Column 91-94; 186PP; English.</p> <p>CC AAW25136 represents a Ricin A-chain Ribosome Inhibitory protein (RIP) which was engineered to contain a selectively removable internal peptide linker sequence separating the alpha and beta units of the RIP. When separated the two units regain activity and are capable of inactivating eukaryotic ribosomes and hence preventing protein production. Many different RIPS may be produced with an internal linker including Trichosanthin, Ricin A-chain, Abrin-A A chain and Saporin. The RIPS can be used in the construction of therapeutic toxins targeted to specific cells such as tumour cells via the attachment of a targeting polypeptide, e.g. monoclonal antibody. A further use is in HIV therapy (see US486903). There is interest in expressing RIP recombinantly in host eukaryotic cells, because of the capacity to provide correct post-translational processing. However, RIPS effectively inhibit protein synthesis in eukaryotic cells resulting in cell death. Since the inactive RIP proteins are not cytotoxic to eukaryotic cells, they can be recombinantly expressed in such cells and then converted to active RIP proteins. (Updated on 25-MAR-2003 to correct PF field.)</p>	<p>PT PT LX Hey TD, Morgan AER, Walsh TA; I1 WPI: 1997-362934/33.</p> <p>CX DNA encoding pro-ribosome inactivating proteins - inactive PT precursors of ribosome inactivating proteins; can be expressed in eukaryotic cells without causing cell death</p> <p>CX Claim 4; Column 91-94; 186PP; English.</p> <p>CC AAW25136 represents a Ricin A-chain Ribosome Inhibitory protein (RIP) which was engineered to contain a selectively removable internal peptide linker sequence separating the alpha and beta units of the RIP. When separated the two units regain activity and are capable of inactivating eukaryotic ribosomes and hence preventing protein production. Many different RIPS may be produced with an internal linker including Trichosanthin, Ricin A-chain, Abrin-A A chain and Saporin. The RIPS can be used in the construction of therapeutic toxins targeted to specific cells such as tumour cells via the attachment of a targeting polypeptide, e.g. monoclonal antibody. A further use is in HIV therapy (see US486903). There is interest in expressing RIP recombinantly in host eukaryotic cells, because of the capacity to provide correct post-translational processing. However, RIPS effectively inhibit protein synthesis in eukaryotic cells resulting in cell death. Since the inactive RIP proteins are not cytotoxic to eukaryotic cells, they can be recombinantly expressed in such cells and then converted to active RIP proteins. (Updated on 25-MAR-2003 to correct PF field.)</p>
<p>Sequence 290 AA;</p> <p>Query Match 97.9%; Score 955; DB 18; Length 290; Best Local Similarity 95.0%; Pred. No. 4.1e-94; Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;</p> <p>CC 2 IFPKQYPIINFTAGATVOSYTNFTRAVRGLT-----VLPNRVGLPQNRFILY 51 25 IFPKQYPIINFTAGATVOSYTNFTRAVRGLTGADRVHEIPVLPNRVGLPQNRFILY 84</p> <p>52 ELSNHAEISVTLADTVNAYVGTRAGNSAYFFHDNQEAEATHLFTDVQNYTFARG 111 85 ELSNHAEISVTLADTVNAYVGTRAGNSAYFFHDNQEAEATHLFTDVQNYTFARG 144</p> <p>112 GNYDRLQLAGNLRENIELGNGPLEEAISALLYYSTGGTOLPTLARSFICIONISEAAR 171 145 GNYDRLQLAGNLRENIELGNGPLEEAISALLYYSTGGTOLPTLARSFICIONISEAAR 204</p> <p>172 FQYIEGMRTRIRYRNRS 190 205 FQYIEGMRTRIRYRNRS 223</p>	<p>Query Match 97.9%; Score 955; DB 18; Length 290; Best Local Similarity 95.0%; Pred. No. 4.1e-94; Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;</p> <p>CC 2 IFPKQYPIINFTAGATVOSYTNFTRAVRGLT-----VLPNRVGLPQNRFILY 51 25 IFPKQYPIINFTAGATVOSYTNFTRAVRGLTGADRVHEIPVLPNRVGLPQNRFILY 84</p> <p>52 ELSNHAEISVTLADTVNAYVGTRAGNSAYFFHDNQEAEATHLFTDVQNYTFARG 111 85 ELSNHAEISVTLADTVNAYVGTRAGNSAYFFHDNQEAEATHLFTDVQNYTFARG 144</p> <p>172 FQYIEGMRTRIRYRNRS 190 205 FQYIEGMRTRIRYRNRS 223</p>
<p>RESULT 4 AAW21699 ID AAW21699 standard; Protein; 290 AA. AC AAW21699; XX DE Ricin A-chain RIP.</p> <p>XX pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer; inactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell. XX Ricinus communis.</p>	<p>RESULT 5 AAP70097 ID AAP70097 standard; protein; 332 AA. AC AAP70097; XX DE Ricin A. XX Key PH Region FT Qualifiers 152-162</p>



DT	13-AUG-1990	(first entry)	QY	172	FQVIEGEMRTRTRYNRRSA 190
XX	Ricin A	encoded by insert from plasmid pRA123.	Db	216	FQVIEGEMRTRTRYNRRSA 234
XX	Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.				
XX	Ricinus communis.				
OS	Synthetic.				
XX					
PH	Key	Location/Qualifiers	XX	172	FQVIEGEMRTRTRYNRRSA 190
FT	Peptide	1..35	AC	216	FQVIEGEMRTRTRYNRRSA 234
FT	Peptide	/label= leader sequence	XX		
FT	Peptide	36..302	XX		
FT	Peptide	/label=A-chain	XX		
FT	Peptide	303..314	XX		
FT	Peptide	/label=linker	XX		
FT	Peptide	315..332	XX		
XX	EP335476-A.	/label=B-chain	XX		
PN			XX		
XX			OS		
PD	04-OCT-1989.		Synthetic.		
XX			XX		
PF	19-JAN-1989;	89EP-0201162.	XX		
XX			XX		
PR	08-FEB-1984;	84US-0578115.	XX		
PR	08-FEB-1984;	84US-0578121.	XX		
PR	09-FEB-1984;	84US-0578122.	XX		
PR	07-SEP-1984;	84US-0648759.	XX		
PR	20-SEP-1984;	84US-0653315.	XX		
XX	(CETU ) CETUS CORPORATION.		XX		
XX	Gelfand D, Lawyer FC, Horn G, Greenfield L, Nitecki D, Kaplan D;		XX		
PI	PIatak MG;		XX		
XX	WPI; 1989-286959/40.		XX		
DR	N-PSDB; AAN91281.		XX		
XX			XX		
PT	Recombinant vectors expressing ricin chains or diphtheria toxin -used for		XX		
PT	prodn. of new immunotoxin conjugates with monoclonal antibodies, having		XX		
PT	high cell specificity and good extracellular stability.		XX		
XX			XX		
PS	Disclosure; Fig 14; 54pp; English.		XX		
XX	CC Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for		XX		
CC	ricin A, as well as codons for A to the B chain.		XX		
CC	Following modification for ease of manipulation the plasmid was used to		XX		
CC	construct expression vectors which express the conjugates in		PA		
CC	host cells.		XX		
CC	(Updated on 31-OCT-2002 to add missing OS field.)		PI		
CC	(Updated on 25-MAR-2003 to correct PF field.)		XX		
CC	(Updated on 25-MAR-2003 to correct PR field.)		DR		
XX	(Updated on 25-MAR-2003 to correct PI field.)		XX		
SQ	Sequence 332 AA;		XX		
Query Match	97.9%	Score 955; DB 10; Length 332;			
Best Local Similarity	95.0%	Best No. 4..9e-94;			
Matches	189; Conservative	0; Mismatches 0; Indels 10; Gaps 1;			
QY	2 IFPKQYPIINFTTGTATVQSYTNFTRAVGRILT-----VLPNRVGLPQNQRFLIV 51		PS		
Db	36 IFPKQYPIINFTTGTATVQSYTNFTRAVGRILTGADRVHEIPVLPNRVGLPQNQRFLIV 95		XX		
QY	52 ELSNEAELSTVLADLVTDVNAVTVGTRAGNSAYFFHDNQEDEAITHLFTDVQNYTFAG 111		CC		
Db	96 ELSNEAELSTVLADLVTDVNAVTVGTRAGNSAYFFHDNQEDEAITHLFTDVQNYTFAG 155		CC		
QY	112 GNYDLEQLAGNLRENIELNGNPLEEASALYYYSTGGTOLPLARSFTICIONISEAR 171		CC		
Db	156 GNYDLEQLAGNLRENIELNGNPLEEASALYYYSTGGTOLPLARSFTICIONISEAR 215		CC		
QY	112 GNYDLEQLAGNLRENIELNGNPLEEASALYYYSTGGTOLPLARSFTICIONISEAR 171		CC		
Db	156 GNYDLEQLAGNLRENIELNGNPLEEASALYYYSTGGTOLPLARSFTICIONISEAR 215		CC		
Query Match	97.9%	Score 955; DB 16; Length 554;			
Best Local Similarity	95.0%	Pred. No. 9..e-94;			
Matches	189; Conservative	0; Mismatches 0; Indels 10; Gaps 1;			

Qy	2 IFPKQYPIINFTTAGATVQSYTNPRAVGRLL-----VLPNRVGLPINQRFLV 51	Db	96 ELSNHAESTVTLDVTNAVVGYRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFG 155
Db	278 IFPKQYPIINFTTAGATVQSYTNPRAVGRLLGADVRHEIPLPNRVGLPINQRFLV 337	Qy	112 GNDRLQLAGNRENTIELNGPLEEAISALYYSTGGTQLPTLARSFTICIQMISEAR 171
Qy	52 ELSNHAELSVTLLDVTNAVVGYRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFG 111	Db	156 GNDRLQLAGNRENTIELNGPLEEAISALYYSTGGTQLPTLARSFTICIQMISEAR 215
Db	338 ELSNHAELSVTLLDVTNAVVGYRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFG 397	Qy	172 FOYIEGEMTRTRYNRSAA 190
Qy	112 GNDRLQLAGNRENTIELNGPLEEAISALYYSTGGTQLPTLARSFTICIQMISEAR 171	Db	216 FOYIEGEMTRTRYNRSAA 234
Db	398 GNDRLQLAGNRENTIELNGPLEEAISALYYSTGGTQLPTLARSFTICIQMISEAR 457	RESULT 10	
Qy	172 FOYIEGEMTRTRYNRSAA 190	DB	AAP50166 standard; Protein; 565 AA.
Db	458 FOYIEGEMTRTRYNRSAA 476	ID	AAP50166;
		XX	
		AC	AAP50166;
		XX	
		DT	16-OCT-1991 (first entry)
		XX	
		DE	Sequence of preproricin encoded by preU617.
		XX	
		KW	Toxin; anti-tumour therapy.
		XX	
		OS	Ricinus.
		XX	
		FH	Location/Qualifiers
		Key	
		Peptide	1..24
		FT	/label= signal
		FT	25..565
		Protein	
		Region	292..303
		FT	/label= links the C-terminus of the A chain and
		FT	the N-terminus of the B chain
		FT	
		Modified-site	34..36
		FT	/label= N-linked glycosylation
		FT	260..262
		FT	
		Modified-site	292..303
		FT	/label= N-linked glycosylation
		FT	
		Modified-site	398..400
		FT	/label= N-linked glycosylation
		FT	
		Modified-site	438..440
		FT	/label= N-linked glycosylation
		XX	
		EP145111-A.	
		XX	
		DD	19-JUN-1985.
		XX	
		PP	13-JUL-1984;
		XX	
		PR	13-MAR-1984;
		PR	15-JUL-1983;
		PR	15-JUL-1983;
		XX	83CH-0019265.
		(UYWA-)	UNIV WARWICK.
		XX	
		Lord JM,	Roberts LM,
		PA	Lamb ET;
		XX	
		DR	WPI: 1985-148046/25.
		XX	N-PSDB; AAN50202.
		AX	
		PT	New DNA sequences coding for ricin type plant toxin - or its
		PT	mutants, and modified vectors and host microorganisms
		XX	
		PS	disclosure; Page 30-30c; 40pp; English.
		XX	
		Query Match	97.9%; Score 955; DB 10; Length 562;
		Best Local Similarity	95.0%; Pred. No. 1e-93;
		Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;	
Qy	2 IFPKQYPIINFTTAGATVQSYTNPRAVGRLL-----VLPNRVGLPINQRFLV 51	CC	Proricin is the whole polypeptide encoded by AAN50202 and the DNA
CC	CC	encoding this is claimed. Proricin is obtained from proproricin by	
CC	CC	removal of the AA leader sequence. The linker AA sequence which is	
CC	CC	present in the precursor polypeptide is enzymatically removed in the	
CC	CC	cell to separate the A and B chains, which are joined by a	
CC	CC	disulphide bridge during the formation of the ricin molecule itself.	
CC	CC	This linker region as well as the presumptive amino terminal leader	
CC	CC	or signal sequence are not present in the sequences already	
CC	CC	published by Funatsu et al.	
Qy	52 ELSNHAELSVTLLDVTNAVVGYRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFG 111		
Db	36 IFPKQYPIINFTTAGATVQSYTNPRAVGRLLGADVRRLTGADVREIPVLPNRVGLPINQRFLV 95		
Qy	52 ELSNHAELSVTLLDVTNAVVGYRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFG 111		

XX SQ Sequence 565 AA;  
 Query Match 97.9%; Score 955; DB 6; Length 565;  
 Best Local Similarity 95.0%; Pred. No. 1e-93 ;  
 Matches 189; Conservative 0; Mismatches 10; Gaps 1;  
 Indels 10;

Qy 2 IIPKQYPIINFATAGATQSYNTNFIRAVRGRIT-----VLDNRYGLPINQBETFLY 51  
 Db 25 IIPKQYPIINFATAGATQSYNTNFIRAVRGRITGADYVRHDIPVLPRVGLPINQFILY 84

Qy 52 ELSNHAEISVTIALDVTNAYVGYRAGNSAYFFPDNQEDAAITHLFTDVNRYYFAFG 111  
 Db 85 ELSNHAEISVTIALDVTNAYVGYRAGNSAYFFPDNQEDAAITHLFTDVNRYYFAFG 144

Qy 112 GNDRLBLAGNIRENTELGNGLPLEEATSLVYXSTGETQLPTLARSFIICIQMISEAAR 171  
 Db 145 GNDRLBLAGNIRENTELGNGLPLEEATSLVYXSTGETQLPTLARSFIICIQMISEAAR 204

Qy 172 FQYIEGEMTRTRYNRSAA 190  
 Db 205 FQYIEGEMTRTRYNRSAA 223

RESULT 11  
 AAG78300 standard; Protein: 565 AA.  
 XX AC AAG78300;  
 XX DT 15-NOV-2001 (first entry)  
 XX DE Castor bean preproricin protein (SEQ ID 1).  
 XX KW Castor bean plant; preproricin; ricin; A chain; B chain;  
 KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;  
 KW retroviral infection; anti-HIV; virucide activity; viral protease.  
 XX OS Ricinus communis.

XX FH Key Location/Qualifiers  
 FT Peptide 1..24  
 FT Protein /label= Signal peptide  
 FT /label= Ricin\_A\_chain  
 /note= "N-glycosidase"  
 FT Peptide 25..290  
 FT /label= Linker\_Peptide  
 /note= "Cleaved during activation of ricin"  
 FT Protein 303..565  
 FT /label= Ricin\_B\_chain  
 /note= "Galactose/N-acetylgalactosamine-binding lectin"  
 PN WO200160393-A1.  
 XX PD 23-AUG-2001.  
 XX PF 15-FEB-2001; 2001WO-US05282.  
 XX PR 16-FEB-2000; 2000US-0182759.  
 XX PA (BECH-) BECHTEL BWXT IDAHO LLC.  
 XX PI Keener WK, Ward TE;  
 DR WPI; 2001-581908/65.  
 DR N-PSDB; AAI64137.  
 XX PT Novel composition comprising toxin e.g. ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.  
 XX Disclosure; Page 47-50; 66pp; English.

XX CC The sequence relates to preproricin protein encoded by the DNA sequence given in AAI64137. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the viral genome thereby preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem. The agent enters the virus cell and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell until degraded in it, unless the cell is infected with the virus, where the viral protease activates it.

XX SQ Sequence 565 AA;  
 Query Match 97.9%; Score 955; DB 22; Length 565;  
 Best Local Similarity 95.0%; Pred. No. 1e-93 ;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy 2 IIPKQYPIINFATAGATQSYNTNFIRAVRGRIT-----VLDNRYGLPINQFILY 51  
 Db 25 IIPKQYPIINFATAGATQSYNTNFIRAVRGRITGADYVRHDIPVLPRVGLPINQFILY 84

Qy 52 ELSNHAEISVTIALDVTNAYVGYRAGNSAYFFPDNQEDAAITHLFTDVNRYYFAFG 111  
 Db 85 ELSNHAEISVTIALDVTNAYVGYRAGNSAYFFPDNQEDAAITHLFTDVNRYYFAFG 144

Qy 112 GNDRLBLAGNIRENTELGNGLPLEEATSLVYXSTGETQLPTLARSFIICIQMISEAAR 171  
 Db 145 GNDRLBLAGNIRENTELGNGLPLEEATSLVYXSTGETQLPTLARSFIICIQMISEAAR 204

Qy 172 FQYIEGEMTRTRYNRSAA 190  
 Db 205 FQYIEGEMTRTRYNRSAA 223

RESULT 12  
 AAG78304 standard; Protein: 565 AA.  
 XX AC AAG78304;  
 XX DT 27-NOV-2001 (first entry)  
 XX DE Modified castor bean preproricin (SEQ ID 10).  
 XX DE Castor bean plant; preproricin; ricin; A chain; B chain;  
 KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;  
 KW retroviral infection; anti-HIV; virucide activity; viral protease.  
 XX OS Ricinus communis  
 XX OS Chimeric - Human immunodeficiency virus type 2.  
 XX OS Chimeric - Human immunodeficiency virus type 2.

XX FH Key Location/Qualifiers  
 FT Peptide 1..24  
 FT Protein /label= Signal\_peptide  
 FT /label= Ricin\_A\_chain  
 /note= "N-glycosidase"  
 FT Peptide 25..302  
 FT /label= Linker\_Peptide  
 /note= "Cleaved during activation of ricin"  
 FT Protein 303..565  
 FT /label= Ricin\_B\_chain  
 /note= "Galactose/N-acetylgalactosamine-binding lectin"  
 PN WO200160393-A1.  
 XX PD 23-AUG-2001.  
 XX PF 15-FEB-2001; 2001WO-US05282.  
 XX PR 16-FEB-2000; 2000US-0182759.  
 XX PA (BECH-) BECHTEL BWXT IDAHO LLC.  
 XX PI Keener WK, Ward TE;  
 DR WPI; 2001-581908/65.  
 DR N-PSDB; AAI64137.  
 XX PT Novel composition comprising toxin e.g. ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.  
 XX Disclosure; Page 47-50; 66pp; English.

XX CC /note= "Protein consists of the ricin A chain, a linker peptide, and the ricin B chain. Proricin is proteolytically cleaved between the A chain and the linker to yield mature ricin"  
 /label= Ricin\_A\_chain  
 /note= "N-glycosidase"  
 /label= Linker\_peptide  
 /label= Cleavage-site

XX PT 292..303  
 FT /label= Linker\_peptide  
 FT Cleavage-site  
 FT 296..297

	/label= HIV_protease_cleavage_site
	304...565
	/label= Ricin_B_Chain
	/note= "Galactose/N-acetylgalactosamine-binding lectin"
Protein	WO200160393_A1;
XX	PR
XX	23-AUG-2001.
XX	15-FEB-2001; 2000US-0182759.
XX	16-FEB-2000; 2000US-0182759.
XX	(BECCH-) BECTEL BXKT IDAHO LLC.
PA	Keener WK, Ward TE;
XX	WPI; 2001-581908/65.
XX	DR N-PSDB; AAI64445.
XX	Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.
XX	Example 1: Page 59-63; 66pp; English.
XX	The sequence relates to the amino acid sequence of a modified preproricin protein encoded by AA64145. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virusicidal activities. The agent is able to enter all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell unless the cell is infected with the HIV virus, where the viral protease activates it. Ricin's mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem.
XX	Sequence 565 AA;
SQ	Query Match 97.9%; Score 955; DB 22; Length 565; Best Local Similarity 95.0%; Pred. No. 1e-93; 0; Mismatches 0; Indels 10; Gaps 189; Conservative 0;
Qy	2 IFPKQPIINFTAGATVQSYTNIFIRAVRGLRT-----VLPNVRGLPQNQRFLIV 51
Db	25 IFPKQPIINFTAGATVQSYTNIFIRAVRGRUTTGADYRHE1PVLPNVRGLPQNQRFLIV 84
Qy	52 ELSNHAEELSVTLADTVNAYVYGRAGNSAYFHPDNQDAEITHLFDVQNRYTFAGF 11
Db	85 ELSNHAEELSVTLADTVNAYVYGRAGNSAYFHPDNQDAEITHLFDVQNRYTFAGF 14
Qy	112 GNYDRLEQLAGNIRENTLGNGPLEEAISALYYSTGCTQLPITLARSFLICIONISEAR 17
Db	145 GNYDRLEQLAGNIRENTLGNGPLEEAISALYYSTGCTQLPITLARSFLICIONISEAR 21
Qy	172 FQYIEGEMTRIYNRRSA 190
Db	205 FQYIEGEMTRIYNRRSA 223
RESULT 13	AAP70326
ID	AAP70326 standard; Protein; 576 AA.
XX	AAP70326;

DT	25-MAR-2003	(updated)	
DT	21-MAY-1991	(first entry)	
XX	Sequence of Ricinus communis (castor bean) Ricin toxin		
DE	DB (RT or ricin) B precursor encoded by pR138.		
XX	Lectin; toxin protein; cytotoxic; cytostatic; castor bean; plant toxin.		
KW			
KW			
XX	Ricinus communis.		
OS			
XX			
Key		Location/Qualifiers	
FH		1..35	
FT Region		/note= "leader"	
FT Region		36..302	
FT Region		/note= "A-chain"	
FT Region		315..516	
FT Region		/note= "B-chain"	
XX			
PN	EP237676-A.		
XX			
PD	23-SEP-1987.		
XX			
PF	13-NOV-1986;	86EP-0308877.	
XX			
PR	07-MAR-1986;	86US-0837583.	
XX			
PA	(CETU ) CETUS CORP.		
PA	(CHIR ) CHIRON CORP.		
XX			
PI	Piatak M;		
XX			
DR	WPI:1987-265177/38.		
DR	N-PSDB; AAN70526.		
XX			
PT	New non-glycosylated ricin precursor and toxin etc. - are by recombinant DNA procedures with specific isolation step		
PT	purified and soluble prods.		
XX			
PS	Disclosure: Fig 14(1-2); 112pp; English.		
XX			
CC	The full length sequences encoding ricin A (AAN70520), ricin B (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) were obtained, using the messenger RNA to obtain a cDNA library, then probing the library to retrieve the desired cDNA insert. The library was probed using the 35-mer given in AAN70514. Figure AAN70520, AAN70521, AAN70522, shows the nucleotide sequence of the inserts obtained by probing a cDNA library containing cDNA inserts obtained by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an ATG start codon and a site at the beginning of the mature protein, (see AAN70518) coding sequences of the inserts can be ligated into expression vectors containing the PhoA promoter-operator and leader sequence (AAN70523) and suitable retroregulators.		
CC	(AAN70523) and suitable retroregulators.		
CC	(Updated on 25-MAR-2003 to correct PA field.)		
XX			
SQ	Sequence 576 AA;		
Query Match	97.9%	Score 955; DB 8; Length 576	
Best Local Similarity	95.0%;	Pred. No. 1e-93; Mismatches 0; Indels	
Matches 189; Conservative 0;			
Qy			
2 IFPKQYPIINFTTAGTVQSNTNPIRAVGRIT-----VLPNRV			
Db	36 IFPKQYPIINFTTAGTVQSNTNPIRAVGRITGADYRHEIPVLPNRY		
Qy	52 ELSNRHAEELSYTLLDVTNAAVVGYRAGNSAYFFHDNQDAAEATHLFT		
Db	96 ELSNRHAEELSYTLLDVTNAAVVGYRAGNSAYFFHDNQDAAEATHLFT		
Qy	112 GMYDLEQIAGNLRNENIEQNGPYLEEAISALIYXSTGTCQLPLTARSTI		

156 GNYDRQELAGNLRNIELNGP, LEAISALYYSTGGTQLPTLARSFTICQMSSEAR 215  
172 FOYIEGEMTRIRYRNRSA 190  
216 FOYTBGEMTRIRYRNRSA 234

delivery of agents (e.g. therapeutic genes, toxins, detectable labels) into cells. The use of a translocation mechanism ensures that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a single hybrid recombinant protein, permitting reproducibility, consistency, and the precise control of composition.

RESULT 14  
AAW25787 AAW25787 standard: protein: 576 AA.

AAW25787;

25-MAR-2003 (updated)  
27-MAR-1998 (first entry)

Castorbean ricin.

Ricin; cytotoxin; hybrid protein; cell delivery;  
cysteine binding ligand; translocation domain; diphtheria toxin B';  
interleukin-2; T-cell lymphoma; organ rejection; therapy.

Ricinus communis.

Key Peptide	Location/Qualifiers
1..35	Peptidase inhibitor domain

Protein 36 / 1a

Peptide	303..314
Domain	315..576
	/label=Linker

卷之三

N X US5668255-A.  
D 16-SEP-1997.

X F X 04-AUG-1993; 93US

R 27-JUN-1991; 91US-0722484.  
R 07-JUN-1984; 84US-0618199.

R R R

R R X 14-JUN-1990; 90US-  
R R X 04-AUG-1993; 93US-

( SERA - ) SERAGEN INC

Murphy JR; WPI: 1997-470103/43

N-PSDB; AAT91638.

New hybrid mRECQL binding domain of a translocation domain

Example 4; Fig 11A-

This polypeptide contains DNA (see AAT91638).

of the A-to-B linkage ricin-diphtheria toxin-E. coli. The hybrid

conditions involving such as certain T- $\alpha$  cases. The hybrid

target cells. Clari-

CC domain and a cell binding or polypeptide toxic

XX Example 4; Fig 11; 31pp; English.

PS XX The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein selected from diphtheria toxin, botulinum neurotoxin, ricin, cholera toxin, LT toxin, C3 toxin, shiga-like toxin, pertussis toxin and tetanus toxin, which translocate the third part of the across the cytoplasmic membrane into the cytosol of the cell; and (c) the third part comprises a polypeptide entity to be introduced into the cell which is non-native to the naturally occurring protein of (b). This sequence represents the Castor bean ricin toxin sequence for use in generating the hybrid of the invention. The hybrid molecule enables the direction of appropriate therapy to affected cells, allowing them to function properly and alleviate or cure the disease. The hybrid is especially used in treating genetic deficiency diseases, by delivering to affected cells an enzyme supplying the missing function, to supplementing cellular levels of a particular enzyme or a scarce precursor or cofactor, to directing toxins or other poisons to destroy particular cells (such as adipocytes, cancer cell, or virus infected-cells), to counteracting viral infections such as HIV, by introducing appropriate antibodies to viral proteins. It is also involved in the process of getting non-therapeutic substances such as detectable labels into cells.

XX	Sequence	576 AA;	Score 955; DB 20; Length 576;	Best Local Similarity 95.0%; Pred. No. 1e-93;	Mismatches 0;	Indels 10;	Gaps 1;
Qy	2	IPPKQYPLINFTTAGATQSYTNFIRAVGRIT-----VLENRGLPINQRFILV	51				
Db	36	IPPKQYPLINFTTAGATQSYTNFIRAVGRITGADVRHLPVLPNRYGPINQRFILV	95				
Qy	52	ELSNHAELSVTIALDVTNAVYVYGRAGNSAYFHPDNQEDAIAITHLFTDVNRYTFAG	111				
Db	96	ELSNHAELSVTIALDVTNAVYVYGRAGNSAYFHPDNQEDAIAITHLFTDVNRYTFAG	155				
Qy	112	GNYDRLEGAGLNRLRENIELNGPLEEALSALYYSTGGTQLPTLARSFLICMISEAAR	171				
Db	156	GNYDRLEGAGLNRLRENIELNGPLEEALSALYYSTGGTQLPTLARSFLICMISEAAR	215				
Qy	172	FQYIEGEMRTRIYNRSAA	190				
Db	216	FQYIEGEMRTRIYNRSAA	234				

Search completed: February 10, 2004, 16:22:29  
Job time : 32.3944 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 16:18:30 / Search time 10.9859 Seconds  
(without alignments)  
731.761 Million cell updates/sec

Title: US-10-083-336A-11

Perfect score: 975  
Sequence: 1 MIFPKQYPIINFTAGATVQ.....RFQYIEGMRTRIYNRSA 190

Scoring table: BLOSUM62

Gapext 0.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:

328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	960	98.5	268	2	US-08-356786-8	Sequence 8, Appli
2	960	98.5	534	2	US-08-356786-10	Sequence 10, Appli
3	955	97.9	267	1	US-07-901-707-1	Sequence 1, Appli
4	955	97.9	267	1	US-07-988-430-1	Sequence 1, Appli
5	955	97.9	267	1	US-08-425-336-1	Sequence 1, Appli
6	955	97.9	267	1	US-08-488-113B-1	Sequence 1, Appli
7	955	97.9	267	1	US-08-477-484B-1	Sequence 1, Appli
8	955	97.9	267	2	US-08-646-360-1	Sequence 1, Appli
9	955	97.9	267	3	US-08-839-765-1	Sequence 1, Appli
10	955	97.9	267	3	US-09-136-336-1	Sequence 1, Appli
11	955	97.9	267	4	US-09-610-838-1	Sequence 1, Appli
12	955	97.9	267	5	PCT-US92-09487-1	Sequence 1, Appli
13	955	97.9	290	1	US-08-485-286-27	Sequence 27, Appli
14	955	97.9	290	1	US-08-485-286-27	Patent No. 5248666
15	955	97.9	290	6	5248666-4	Sequence 16, Appli
16	945	96.9	267	1	US-08-218-303-16	Sequence 61, Appli
17	945	96.9	267	2	US-08-338-793D-61	Sequence 1, Appli
18	945	96.9	267	4	US-09-538-873-1	Sequence 1, Appli
19	865.5	88.8	540	1	US-08-378-761A-77	Sequence 77, Appli
20	865.5	88.8	540	1	US-08-485-286-77	Sequence 6, Appli
21	336	34.5	247	1	US-08-488-113B-6	Sequence 6, Appli
22	336	34.5	247	1	US-08-477-484B-6	Sequence 6, Appli
23	336	34.5	247	2	US-08-646-336-0-6	Sequence 6, Appli
24	336	34.5	247	3	US-08-839-765-6	Sequence 6, Appli
25	336	34.5	247	4	US-09-610-838-6	Sequence 6, Appli
26	336	34.5	247	1	US-08-378-761A-74	Sequence 74, Appli
27	336	34.5	267	1	US-08-378-761A-74	Sequence 74, Appli

RESULT 1  
US-08-356-786-8  
Sequence 8, Application US/08356786  
Patent No. 5248666  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEES: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPILER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,786  
FILING DATE:  
CLASIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CRP-053  
FILING DATE: 07/8/31, 967  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7100  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 268 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-786-8

Query Match 98.5%; Score 960; DB 2; Length 268;

Best Local Similarity 95.0%; Pred. No. 2.5e-103;

Indels 10; Gaps 0; Mismatches 0;

Matches 190; Conservative 0;

Sequence 74, Appli

QY 1 MIFPKQPIINFTAGATVOSYTINPIRAVRGLT-----VLPNRVGLPINQRFIL 50  
 Db 1 MIFPKQPIINFTAGATVOSYTINPIRAVRGLTGADRVRLTGTADTRHEIIVLPNFGLPINQRFIL 60  
 Qy 51 VELSNHAELSVTLALDVINAYVVGAGRNSAYFFPFDNQEDAETHLFTDQNRYTFAP 110  
 Db 61 VELSNHAELSVTLALDVINAYVVGAGRNSAYFFPFDNQEDAETHLFTDQNRYTFAP 120  
 Qy 111 GNYDRLEQLAGNLRENTLGNGPLEEASALYYSTGGTQLPTLARSFIICIQMISEAA 170  
 Db 121 GNYDRLEQLAGNLRENTLGNGPLEEASALYYSTGGTQLPTLARSFIICIQMISEAA 180

RESULT 2  
 US-08-356-786-10  
 i Sequence 10 , Application US/08356786  
 i GENERAL INFORMATION:  
 i i APPLICANT: Huston, James S.  
 i i ADDRESS: Oppermann, Hermann  
 i i i Houston, L. L.  
 i i APPLICANT: Ring, David B.  
 i i i Bicknell  
 i i TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
 i i NUMBER OF SEQUENCES: 16  
 i i CORRESPONDENCE ADDRESS:  
 i i ADDRESS: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault  
 i i STREET: Exchange Place, 53 State Street  
 i i CITY: Boston  
 i i STATE: Massachusetts  
 i i COUNTRY: USA  
 i i ZIP: 02109

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC Compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 COMPUTER: IBM PC Compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/356,786  
 FILING DATE: 04-NOV-1991

CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/831,967  
 FILING DATE: 06-FEB-1992

ATTORNEY/AGENT INFORMATION:  
 NAME: Pitcher, Edmund R.  
 REGISTRATION NUMBER: 27,829  
 REFERENCE/DOCKET NUMBER: CRP-053

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 248-7100  
 TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 534 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-356-786-10

Qy 63 VELSNHAELSVTLALDVINAYVVGAGRNSAYFFHDPDQEDAETHLFTDQNRYTFAP 122  
 Qy 111 GNYDRLEQLAGNLRENTLGNGPLEEASALYYSTGGTQLPTLARSFIICIQMISEAA 170  
 Db 123 GNYDRLEQLAGNLRENTLGNGPLEEASALYYSTGGTQLPTLARSFIICIQMISEAA 182  
 Qy 171 RFQYIEGMRTRIYNRSA 190  
 Db 183 RFQYIEGMRTRIYNRSA 202

RESULT 3  
 US-07-901-707-1  
 i Sequence 1, Application US/07901707  
 i GENERAL INFORMATION:  
 i i APPLICANT: Bernard, Susan L.  
 i i ADDRESS: Better, Marc D.  
 i i APPLICANT: Carroll, Steve F.  
 i i APPLICANT: Lane, Julie A.  
 i i TITLE OF INVENTION: Materials Comprising and Methods of  
 i i Composition and Use for Ribosome-Inactivating Proteins  
 i i NUMBER OF SEQUENCES: 57  
 i i CORRESPONDENCE ADDRESS:  
 i i ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 i i STREET: Two First National Plaza, 20 South Clark  
 i i CITY: Chicago  
 i i STATE: Illinois  
 i i COUNTRY: USA  
 i i ZIP: 60603  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/901,707  
 FILING DATE: 19920619  
 CLASSIFICATION: 435  

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
 NAME: No. 5376516 and, Grera E.  
 REGISTRATION NUMBER: 35,302  
 REPERIENCE/DOCKET NUMBER: 27129/30910  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 346-5750  
 TELEFAX: (312) 984-5750  
 TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 267 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein

US-07-901-707-1

Query Match 97.9%; Score 955; DB 1; Length 267;  
 Best Local Similarity 95.0%; Pred. No. 9\_4e-103;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy 2 IFPKQYPIINFTAGATVOSYTINPIRAVRGLT-----VLPNRVGLPTNORFLY 51  
 Db 1 IFPKQYPIINFTAGATVOSYTINPIRAVRGLT-----VLPNRVGLPTNORFLY 60

Qy 52 ELSNHAEELSVTLALDVINAYVVGAGRNSAYFFHDPDQEDAETHLFTDQNRYTFAP 111  
 Db 61 ELSNHAEELSVTLALDVINAYVVGAGRNSAYFFHDPDQEDAETHLFTDQNRYTFAP 120

Qy 112 GNYDRLEQLAGNLRENTLGNGPLEEASALYYSTGGTQLPTLARSFIICIQMISEAA 171

Db 121 GNYDRLEQLAGNLRENTIELNGNPLEBAISALYYSTGGTQLPTLARSFLCIMSEAR 180  
 Qy 172 FQYIEGEMTRIYNRSA 190  
 Db 181 FQYIEGEMTRIYNRSA 199

## RESULT 4

US-07-988-430-1

; Sequence 1, Application US/07988430  
 ; Patent No. 5416202  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bernhard, Susan L.  
 ; APPLICANT: Better, Marc D.  
 ; APPLICANT: Carroll, Stephen F.  
 ; APPLICANT: Lane, Julie A.  
 ; APPLICANT: Lei, Shau-Ping  
 ; TITLE OF INVENTION: Materials Comprising and Methods of Preparation and Use for Ribosome-Inactivating Proteins  
 ; NUMBER OF SEQUENCES: 101  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
 ; STREET: Two First National Plaza, 20 South Clark  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In ReLease #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/988,430

FILING DATE: 1992/12/09

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: No. 5416-02and, Greta E.

REGISTRATION NUMBER: 35302

REFERENCE/DOCKET NUMBER: 31133

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEFAX: 25-3856

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-07-988-430-1

Db 112 GNYDRLEQLAGNLRENTIELNGNPLEBAISALYYSTGGTQLPTLARSFLCIMSEAR 171  
 Qy 121 GNYDRLEQLAGNLRENTIELNGNPLEBAISALYYSTGGTQLPTLARSFLCIMSEAR 180  
 Qy 172 FQYIEGEMTRIYNRSA 190  
 Db 181 FQYIEGEMTRIYNRSA 199

## RESULT 5

US-08-425-336-1

; Sequence 1, Application US/08425336  
 ; Patent No. 5621083  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Better, Marc D.  
 ; APPLICANT: Carroll, Stephen F.  
 ; APPLICANT: Studnka, Gary M.  
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins  
 ; TITLE OF INVENTION: Proteins  
 ; NUMBER OF SEQUENCES: 140  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In ReLease #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/425,336  
 ; FILING DATE: 18-APR-1995  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/064,691  
 ; FILING DATE: 12-MAY-1993  
 ; APPLICATION NUMBER: US 07/901,707  
 ; FILING DATE: 19-JUN-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/787,567  
 ; FILING DATE: 04-NOV-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meyers, Thomas C.  
 ; REGISTRATION NUMBER: P-36,989  
 ; REFERENCE/DOCKET NUMBER: 31394  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 311/474-6300  
 ; TELEFAX: 312/474-0448  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 267 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-425-336-1

Query Match 97.9%; Score 955; DB 1; Length 267;  
 Best Local Similarity 95.0%; Pred. No. 9.4e-103;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy 2 IFPKQYPIINFATGATVQSYTNFIRAVGRLT-----VLPNRGLPINQRFLV 51  
 Db 1 IFPKQYPIINFATGATVQSYTNFIRAVGRLTGADVRHEIPVLPNRGLPINQRFLV 60  
 Qy 52 ELSNHAEISVTIALDVTNAYVVGYRAGNSAYFHPDNOEADAITHLFTDVQNRTFAFG 111  
 Db 61 ELSNHAEISVTIALDVTNAYVVGYRAGNSAYFFHDNQEDAITHLFTDVQNRTFAFG 120  
 Qy 112 GNYDRLEQLAGNLRENTIELNGNPLEBAISALYYSTGGTQLPTLARSFLCIMSEAR 171

RESULT 6  
US-08-488-113B-1  
Sequence 1; Application US/08488113B  
Patent No. 5744580  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
ADDRESS: Carroll, Stephen R.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 16-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-1  
QY 121 GNYDRLEQAGNLRENTELGNGLPLEAISALYYSTGGTQPLTARSFLICIQMSEAR 180  
QY 172 FOYIEGMRTRIYNRSA 190  
Db 181 FOYIEGMRTRIYNRSA 199  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
ADDRESS: Carroll, Stephen R.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-1  
QY 52 ELSNHAELSYTLALDVTNAYVVGAGRNSAYFFHPDNQDAEATHLFTDVQNYTFARG 111  
Db 61 ELSNHAELSYTLALDVTNAYVVGAGRNSAYFFHPDNQDAEATHLFTDVQNYTFARG 120  
QY 112 GNYDRLEQAGNLRENTELGNGLPLEAISALYYSTGGTQPLTARSFLICIQMSEAR 171  
Db 121 GNYDRLEQAGNLRENTELGNGLPLEAISALYYSTGGTQPLTARSFLICIQMSEAR 180  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
ADDRESS: Carroll, Stephen R.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-1  
QY 2 IFPKQYPIINFETTAGATVQSYTNFIRAVGRIL-----VLPNRVLGINQRFLY 51  
Db 1 IFPKQYPIINFETTAGATVQSYTNFIRAVGRIL-----VLPNRVLGINQRFLY 60  
Query Match Best Local Similarity 95.0%; Pred. No. 9.4e-103; Mismatches 0; Indels 10; Gaps 1;  
Matches 189; Conservative 0; Score 955; DB 1; Length 267;  
Query Match Sequence ID NO: 1: Information for SEQ ID NO: 1:  
Registration Number: 32,918  
Reference/Docket Number: 11022US07/200-70.P3.C2A  
Sequence Characteristics:  
Length: 267 amino acids  
Type: amino acid  
Topology: linear  
Molecule Type: protein  
US-08-477-484B-1  
Query Match

Best Local Similarity 95.0%; Pred. No. 9.4e-103; Mismatches 0; Indels 10; Gaps 1;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US -0 -646 -360 -1

Query Match Score 955; DB 2; Length 267;  
 Best Local Similarity 95.0%; Pred. No. 9.4e-103;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;  
 ; Query Match Score 97.9%; DB 2; Length 267;  
 Best Local Similarity 95.0%; Pred. No. 9.4e-103;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;  
 ; Query Match Score 97.9%; DB 2; Length 267;

QY 2 IFPKQYPIINFATGATQSYNTFRAVGRLT----VLPNVRGLPINQRFLV 51  
 DB 1 IFPKQYPIINFATGATQSYNTFRAVGRLTGADVRHEIPLNVRGLPINQRFLV 60

QY 52 ELSNHAEISVTLALDVTNAYVGFRAGNSAYFFPDNOEDABAATHLPTDVNRYTFAGF 111  
 DB 61 ELSNHAEISVTLALDVTNAYVGFRAGNSAYFFPDNOEDABAATHLPTDVNRYTFAGF 120

QY 112 GNYDRLEQLAGNLRENTIELNGNPLEEALSALLYXSTGGTOLPLTARSFLICOMISEAR 171  
 DB 121 GNYDRLEQLAGNLRENTIELNGNPLEEALSALLYXSTGGTOLPLTARSFLICOMISEAR 180

QY 172 FOYIEGEMTRTRYNRSAA 190  
 DB 181 FOYIEGEMTRTRYNRSAA 199

RESULT 8  
 US-08-646-360-1  
 Sequence 1, Application US/08646360  
 ; Patent No. 5837491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Better, Marc D.  
 ; ATTORNEY/AGENT INFORMATION:  
 ; APPLICANT: Carroll, Stephen F.  
 ; APPLICANT: Studnika, Gary M.  
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 ; NUMBER OF SEQUENCES: 173  
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 ; STREET: 500 West Madison Street, 34th floor  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,360  
 FILING DATE: 13-MAY-1996  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/053348  
 FILING DATE: 12-MAY-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70-P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 1:  
 LENGTH: 267 amino acids

RESULT 9  
 US-08-839-765-1  
 Sequence 1, Application US/08839765  
 ; Patent No. 6146631  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Better, Marc D.  
 ; ATTORNEY/AGENT INFORMATION:  
 ; APPLICANT: Carroll, Stephen F.  
 ; APPLICANT: Studnika, Gary M.  
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 ; NUMBER OF SEQUENCES: 169  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 ; STREET: 500 West Madison Street, 34th floor  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/839,765  
 FILING DATE: 15-APR-1997,  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/425,336  
 FILING DATE: 18-APR-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/839,765  
 FILING DATE: 12-MAY-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70-P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 1:  
 LENGTH: 267 amino acids

NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70-P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 1:  
 LENGTH: 267 amino acids

NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 11022US09/200-70-P3.C3  
 TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 312/707-8889  
 / TELEFAX: 312/707-9155  
 / TELEX: 650 388-1248  
 / INFORMATION FOR SEQ ID NO: 1:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 267 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: protein  
 / US-08-839-765-1

Query Match 97.9%; Score 955; DB 3; Length 267;  
 Best Local Similarity 95.0%; Pred. No. 9.4e-103;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy	2 IFPKQYPIIINFETTAGATVQSTNFIFAVRGLT-----VLPNRVGLPINQRFLV 51	Db	1 IFPKQYPIIINFETTAGATVQSTNFIFAVRGLT-----VLPNRVGLPINQRFLV 60
Qy	52 ELSNHAELSVTLALDVTNAYVGRAGNSAYFFHPDNQEDAATHLFTDVQNYTFAFG 111	Db	61 ELSNHAELSVTLALDVTNAYVGRAGNSAYFFHPDNQEDAATHLFTDVQNYTFAFG 120
Qy	112 GNYDRLEQLAGNLRENTELNGPLEEAISALYYSTGGTQPLTLSFIIQMSAAR 171	Db	121 GNYDRLEQLAGNLRENTELNGPLEEAISALYYSTGGTQPLTLSFIIQMSAAR 180
Qy	172 FQYIEGEMTRTRYNRSAA 190	Db	181 FQYIEGEMTRTRYNRSAA 199

RESULT 10  
 US-09-136-389-1  
 / Sequence 1, Application US/09136389  
 / Patent No. 6146850  
 / GENERAL INFORMATION:  
 /   APPLICANT: Better, Marc D.  
 /   ADDRESS: Carroll, Stephen F.  
 /   ATTORNEY: Studnika, Gary M.  
 /   TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 /   NUMBER OF SEQUENCES: 173  
 / ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 /   STREET: 500 West Madison Street, 34th floor  
 /   CITY: Chicago  
 /   STATE: Illinois  
 /   COUNTRY: USA  
 /   ZIP: 60661  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patent In Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 /   APPLICATION NUMBER: US/09/136,389  
 /   FILING DATE: 09-DEC-1992  
 /   CLASSIFICATION:  
 /   PRIORITY DATA:  
 /   APPLICATION NUMBER: 08/646,360  
 /   FILING DATE: 13-MAY-1996  
 /   APPLICATION NUMBER: PCT/US94/05348  
 /   FILING DATE: 12-MAY-1994  
 /   APPLICATION NUMBER: US 08/064,691  
 /   FILING DATE: 12-MAY-1993  
 /   APPLICATION NUMBER: US 07/988,430  
 /   FILING DATE: 09-DEC-1992  
 /   PRIORITY DATA:  
 /   APPLICATION NUMBER: US 07/901,707  
 /   FILING DATE: 19-JUN-1992

/ PRIOR APPLICATION DATA:  
 /   APPLICATION NUMBER: US 07//787,567  
 /   FILING DATE: 04-NOV-1991  
 /   ATTORNEY/AGENT INFORMATION:  
 /   NAME: McNicholas, Janet M.  
 /   REGISTRATION NUMBER: 32,918  
 /   REFERENCE/DOCKET NUMBER: 200-70-P4  
 / TELECOMMUNICATION INFORMATION:  
 /   TELEPHONE: 312/707-8889  
 /   TELEFAX: 312/707-9155  
 /   TELEX: 650 388-1248  
 / INFORMATION FOR SEQ ID NO: 1:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 267 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: protein  
 / US-09-136-389-1

Query Match 97.9%; Score 955; DB 3; Length 267;  
 Best Local Similarity 95.0%; Pred. No. 9.4e-103;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy	2 IFPKQYPIIINFETTAGATVQSTNFIFAVRGLT-----VLPNRVGLPINQRFLV 51	Db	1 IFPKQYPIIINFETTAGATVQSTNFIFAVRGLT-----VLPNRVGLPINQRFLV 60
Qy	52 ELSNHAELSVTLALDVTNAYVGRAGNSAYFFHPDNQEDAATHLFTDVQNYTFAFG 111	Db	61 ELSNHAELSVTLALDVTNAYVGRAGNSAYFFHPDNQEDAATHLFTDVQNYTFAFG 120
Qy	172 FQYIEGEMTRTRYNRSAA 190	Db	181 FQYIEGEMTRTRYNRSAA 199

RESULT 11  
 US-09-610-838-1  
 / Sequence 1, Application US/09610838  
 / GENERAL INFORMATION:  
 /   PATENT NO. 6376217  
 /   GENERAL INFORMATION:  
 /   APPLICANT: Better, Marc D.  
 /   APPLICANT: Carroll, Stephen F.  
 /   APPLICANT: Studnika, Gary M.  
 /   TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 /   NUMBER OF SEQUENCES: 173  
 / CORRESPONDENCE ADDRESS:  
 /   ADDRESS: McAndrews, Held & Malloy, Ltd.  
 /   STREET: 500 West Madison Street, 34th floor  
 /   CITY: Chicago  
 /   STATE: Illinois  
 /   COUNTRY: USA  
 /   ZIP: 60661  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patent In Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 /   APPLICATION NUMBER: US/09/610,838  
 /   FILING DATE: 06-JUL-2000  
 /   CLASSIFICATION:  
 /   PRIORITY DATA:  
 /   APPLICATION NUMBER: US/09/136,389  
 /   FILING DATE: 18-AUG-1998  
 /   APPLICATION NUMBER: 08/646,360  
 /   FILING DATE: 13-MAY-1996  
 /   APPLICATION NUMBER: PCT/US94/05348  
 /   FILING DATE: 19-JUN-1992

FILING DATE: 12-MAY-1994  
 PRIORITY APPLICATION DATA:  
   APPLICATION NUMBER: US 08/064,691  
   FILING DATE: 12-MAY-1993  
 PRIORITY APPLICATION DATA:  
   APPLICATION NUMBER: US 07/988,430  
   FILING DATE: 09-DEC-1992  
 PRIORITY APPLICATION DATA:  
   APPLICATION NUMBER: US 07/901,707  
   FILING DATE: 19-JUN-1992  
 PRIORITY APPLICATION DATA:  
   APPLICATION NUMBER: US 07/787,567  
   FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
   NAME: McNicholas, Janet M.  
   REGISTRATION NUMBER: 32,118  
   REFERENCE/DOCKET NUMBER: 200-70-PA  
 TELECOMMUNICATION INFORMATION:  
   TELEPHONE: 312/707-9889  
   TELEFAX: 312/707-9155  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
   LENGTH: 267 amino acids  
   TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 US-09-610-838-1

Query Match 97.9%; Score 955; DB 4; Length 267;  
 Best Local Similarity 95.0%; Pred. No. 9.4e-103;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 2 IFPKQYPIINFTAGATQSYNTFIRAVGRLT-----VLPNRYGLPINQRFLV 51  
 Db 1 IFPKQYPIINFTAGATQSYNTFIRAVGRLTGADVRHEIPVLPNRYGLPINQRFLV 60  
 QY 52 ELSNHAEISVTLALDVTAAYVGVGRNSAYFFHPDQDAEATHLFDTDVNRYTFAG 111  
 Db 61 ELSNHAEISVTLALDVTAAYVGVGRNSAYFFHPDQDAEATHLFDTDVNRYTFAG 120  
 QY 112 GNYDRLEGAGNLRENIELNGNPLEEAISALYYSTGGTQLPLTLARSFTICIONISEAR 171  
 Db 121 GNYDRLEGAGNLRENIELNGNPLEEAISALYYSTGGTQLPLTLARSFTICIONISEAR 180  
 QY 172 FOYIEGERTRTRYNRSAA 190  
 Db 181 FOYIEGERTRTRYNRSAA 199

RESULT 12  
 PCT-US92-09487-1  
 Sequence 1, Application pc/TUS9209487  
 GENERAL INFORMATION:  
   APPLICANT: Bernhard, Susan L.  
   APPLICANT: Better, Marc D.  
   APPLICANT: Carroll, Stephen F.  
   APPLICANT: Lane, Julie A.  
   APPLICANT: Lei, Shau-Ping  
 TITLE OF INVENTION: Materials Comprising and Methods of  
 TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
 NUMBER OF SEQUENCES: 101  
 CORRESPONDENCE ADDRESS:  
   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
   STREET: Bicknell  
   STREET: Two First National Plaza, 20 South Clark  
   STREET: Street  
   CITY: Chicago  
   STATE: Illinois  
   COUNTRY: USA  
 ZIP: 60603  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

RESULT 13  
 US-08-378-761A-27  
 Sequence 27, Application US/08378761A  
 Patent No. 5635384  
 GENERAL INFORMATION:  
   APPLICANT: WALS, TERENCE A  
   APPLICANT: HEY, TIMOTHY D  
   APPLICANT: MORGAN, ALICE ER  
 TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
 PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
   ADDRESSEE: ANDREA T. BORUCKI  
   STREET: 9330 ZIONSVILLE ROAD  
   CITY: INDIANAPOLIS  
   STATE: IN  
   COUNTRY: US  
 ZIP: 46268  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25  
 APPLICATION DATA:  
 FILING DATE: 26-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BORUCKI, ANDREA T  
 REGISTRATION NUMBER: 33651  
 REFERENCE/DOCKET NUMBER: 38272B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (317) 337-4846  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 290 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-378-761A-27

Query Match 97.9%; Score 955; DB 1; Length 290;  
 Best Local Similarity 95.0%; Pred. No. 1..e-102;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy 2 IFPKQYPIINFTTAGATVQSYNTNFRAVRGRLT-----VLPNRVGLPINORFILV 51  
 Db 25 IFPKQYPIINFTTAGATVQSYNTNFRAVRGRLTGADVRGRLLTGA 84

Qy 2 IFPKQYPIINFTTAGATVQSYNTNFRAVRGRLT-----VLPNRVGLPINORFILV 51  
 Db 25 IFPKQYPIINFTTAGATVQSYNTNFRAVRGRLTGADVRGRLLTGA 84

Qy 52 ELSNHAEELSVTLALDVTALVYGYRAGNSAYFFHDNQEDAATHLFTDVNRYTEAFG 111  
 Db 85 ELSNHAEELSVTLALDVTALVYGYRAGNSAYFFHDNQEDAATHLFTDVNRYTEAFG 144

Qy 112 GNYDRLEQLAGNLRENLGNGPLEEASALYYSTGGTQLPTLARSFIICOMISEAAR 171  
 Db 145 GNYDRLEQLAGNLRENLGNGPLEEASALYYSTGGTQLPTLARSFIICOMISEAAR 204

Qy 172 FQYIEGEMTRIRYRNRS 190  
 Db 205 FQYIEGEMTRIRYRNRS 223

RESULT 15  
 5248606-4  
 ; PATENT NO. 5248606  
 ; APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN,  
 ; ALICE E.R.  
 ; TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND  
 ; ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATING  
 ; NUMBER OF SEQUENCES: 49  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/535,636  
 ; FILING DATE: 11-JUN-1990  
 ; SEQ ID NO: 4;  
 ; LENGTH: 290  
 ; 5248606-4

Query Match 97.9%; Score 955; DB 6; Length 290;  
 Best Local Similarity 95.0%; Pred. No. 1..e-102;  
 Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy 2 IFPKQYPIINFTTAGATVQSYNTNFRAVRGRLT-----VLPNRVGLPINORFILV 51  
 Db 25 IFPKQYPIINFTTAGATVQSYNTNFRAVRGRLTGADVRGRLLTGA 84

Qy 52 ELSNHAEELSVTLALDVTALVYGYRAGNSAYFFHDNQEDAATHLFTDVNRYTEAFG 111  
 Db 85 ELSNHAEELSVTLALDVTALVYGYRAGNSAYFFHDNQEDAATHLFTDVNRYTEAFG 144

Qy 112 GNYDRLEQLAGNLRENLGNGPLEEASALYYSTGGTQLPTLARSFIICOMISEAAR 171  
 Db 145 GNYDRLEQLAGNLRENLGNGPLEEASALYYSTGGTQLPTLARSFIICOMISEAAR 204

Qy 172 FQYIEGEMTRIRYRNRS 190  
 Db 205 FQYIEGEMTRIRYRNRS 223

RESULT 14  
 US-08-485-286-27  
 ; Sequence 27, Application US/08485286  
 ; Patent No. 5646026  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WALSH, TERENCE A  
 ; APPLICANT: HEY, TIMOTHY D  
 ; APPLICANT: MORGAN, ALICE ER  
 ; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
 ; PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
 ; TREATMENT, AND A KIT THEREFOR  
 ; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
 ; TREATMENT, AND A KIT THEREFOR  
 ; NUMBER OF SEQUENCES: 81  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ANDREA T. BORUCKI  
 ; STREET: 9330 ZIONSVILLE ROAD  
 ; CITY: INDIANAPOLIS  
 ; STATE: IN  
 ; COUNTRY: US  
 ; ZIP: 46256  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/485,286  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/378761  
 ; FILING DATE: 26-JUN-1995

search completed: February 10, 2004, 16:29:35



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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:26:46 ; Search time 24.507 Seconds  
 (without alignments)  
 1623.314 Million cell updates/sec

Title: US-10-083-336A-11

Perfect score: 975 Sequence: 1 MIFPKQYPIINFTAGATVQ.....RFQYIEGEMRTRIYNRSA 190

Scoring table: BLOSUM62

Gapext: 0.5

Searched:

801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters:

801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications AA: \*

- 1: /cgn2\_6\_ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6\_ptodata/1/pubpaa/PCTUS\_NEW\_PUB.pep:\*
- 3: /cgn2\_6\_ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 4: /cgn2\_6\_ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 5: /cgn2\_6\_ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6\_ptodata/1/pubpaa/PCPTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6\_ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6\_ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 9: /cgn2\_6\_ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6\_ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6\_ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6\_ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6\_ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6\_ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6\_ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6\_ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6\_ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6\_ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Match Length DB ID Description

Result No.	Score	Match Length	DB ID	Description
1	975	100.0	190	12 US-10-083-336A-11 Sequence 11, Appl
2	971	99.6	189	12 US-10-083-336A-6 Sequence 6, Appl
3	966	99.1	188	12 US-10-083-336A-4 Sequence 4, Appl
4	960	98.5	200	12 US-10-083-336A-10 Sequence 10, Appl
5	956	98.1	188	12 US-10-083-336A-8 Sequence 8, Appl
6	956	98.1	199	12 US-10-083-336A-5 Sequence 5, Appl
7	955	97.9	267	12 US-10-127-890-1 Sequence 1, Appl
8	955	97.9	576	12 US-10-083-336A-1 Sequence 1, Appl
9	951	97.5	198	12 US-10-083-336A-3 Sequence 3, Appl
10	945	96.9	267	12 US-10-282-935-1 Sequence 1, Appl
11	945	96.9	267	12 US-10-440-796-1 Sequence 1, Appl
12	941	96.5	198	12 US-10-083-336A-7 Sequence 7, Appl
13	939.5	96.4	185	12 US-10-083-336A-9 Sequence 9, Appl
14	679	69.6	179	12 US-10-083-336A-2 Sequence 2, Appl
15	34.5	247	10 US-09-792-793A-39 Sequence 39, Appl	

Result No.	Score	Match Length	DB ID	Description	Query Match	Best Local Similarity	Score	Length
1	975	100.0	190	12 US-10-083-336A-11 Sequence 11, Appl	100.0%; Pred. No. 1.1e-103;	100.0%; Pred. No. 1.1e-103;	975	190;
2	971	99.6	189	12 US-10-083-336A-6 Sequence 6, Appl	Matches 190; Conservative	0; Mismatches 0;	0;	0;
3	966	99.1	188	12 US-10-083-336A-4 Sequence 4, Appl	1 MIFPKQYPIINFTAGATVQSYNTFIRAVGRQLTIPNVRGLPILNDRFLVLSNHAEL	1 MIFPKQYPIINFTAGATVQSYNTFIRAVGRQLTIPNVRGLPILNDRFLVLSNHAEL	60	60
4	960	98.5	200	12 US-10-083-336A-10 Sequence 10, Appl	1 MIFPKQYPIINFTAGATVQSYNTFIRAVGRQLTIPNVRGLPILNDRFLVLSNHAEL	1 MIFPKQYPIINFTAGATVQSYNTFIRAVGRQLTIPNVRGLPILNDRFLVLSNHAEL	60	60
5	956	98.1	188	12 US-10-083-336A-8 Sequence 8, Appl	1 MIFPKQYPIINFTAGATVQSYNTFIRAVGRQLTIPNVRGLPILNDRFLVLSNHAEL	1 MIFPKQYPIINFTAGATVQSYNTFIRAVGRQLTIPNVRGLPILNDRFLVLSNHAEL	60	60
6	956	98.1	199	12 US-10-083-336A-5 Sequence 5, Appl	1 MIFPKQYPIINFTAGATVQSYNTFIRAVGRQLTIPNVRGLPILNDRFLVLSNHAEL	1 MIFPKQYPIINFTAGATVQSYNTFIRAVGRQLTIPNVRGLPILNDRFLVLSNHAEL	60	60
7	955	97.9	267	12 US-10-127-890-1 Sequence 1, Appl	1 VIALDVTNAVYGYRAGNSAYFFHPDNQEDAEITHLFTDVNRYTFAGFNYDRLQL	1 VIALDVTNAVYGYRAGNSAYFFHPDNQEDAEITHLFTDVNRYTFAGFNYDRLQL	120	120
8	955	97.9	576	12 US-10-083-336A-1 Sequence 1, Appl	1 VIALDVTNAVYGYRAGNSAYFFHPDNQEDAEITHLFTDVNRYTFAGFNYDRLQL	1 VIALDVTNAVYGYRAGNSAYFFHPDNQEDAEITHLFTDVNRYTFAGFNYDRLQL	120	120
9	951	97.5	198	12 US-10-083-336A-3 Sequence 3, Appl	1 VIALDVTNAVYGYRAGNSAYFFHPDNQEDAEITHLFTDVNRYTFAGFNYDRLQL	1 VIALDVTNAVYGYRAGNSAYFFHPDNQEDAEITHLFTDVNRYTFAGFNYDRLQL	120	120
10	945	96.9	267	12 US-10-282-935-1 Sequence 1, Appl	1 AGNLRENIELNGNPLEEALASLYYSTGCTGOLPLTLARSFIICOMISSEAARFOYIEGEMR	1 AGNLRENIELNGNPLEEALASLYYSTGCTGOLPLTLARSFIICOMISSEAARFOYIEGEMR	180	180
11	945	96.9	267	12 US-10-440-796-1 Sequence 7, Appl	1 AGNLRENIELNGNPLEEALASLYYSTGCTGOLPLTLARSFIICOMISSEAARFOYIEGEMR	1 AGNLRENIELNGNPLEEALASLYYSTGCTGOLPLTLARSFIICOMISSEAARFOYIEGEMR	180	180
12	941	96.5	198	12 US-10-083-336A-7 Sequence 9, Appl	1 AGNLRENIELNGNPLEEALASLYYSTGCTGOLPLTLARSFIICOMISSEAARFOYIEGEMR	1 AGNLRENIELNGNPLEEALASLYYSTGCTGOLPLTLARSFIICOMISSEAARFOYIEGEMR	180	180
13	939.5	96.4	185	12 US-10-083-336A-9 Sequence 2, Appl	1 AGNLRENIELNGNPLEEALASLYYSTGCTGOLPLTLARSFIICOMISSEAARFOYIEGEMR	1 AGNLRENIELNGNPLEEALASLYYSTGCTGOLPLTLARSFIICOMISSEAARFOYIEGEMR	180	180
14	679	69.6	179	12 US-10-083-336A-2 Sequence 39, Appl	1 VIALDVTNAVYGYRAGNSAYFFHPDNQEDAEITHLFTDVNRYTFAGFNYDRLQL	1 VIALDVTNAVYGYRAGNSAYFFHPDNQEDAEITHLFTDVNRYTFAGFNYDRLQL	120	120
15	34.5	247	10 US-09-792-793A-39 Sequence 39, Appl	1 VIALDVTNAVYGYRAGNSAYFFHPDNQEDAEITHLFTDVNRYTFAGFNYDRLQL	1 VIALDVTNAVYGYRAGNSAYFFHPDNQEDAEITHLFTDVNRYTFAGFNYDRLQL	120	120	

#### ALIGNMENTS

RESULT 1  
 US-10-083-336A-11  
 ; Sequence 11, Application US/1008336A  
 ; Publication No. US20030181662A1  
 ; GENERAL INFORMATION  
 ; APPLICANT: Millard, Charles B  
 ; APPLICANT: Byrne, Michael P  
 ; APPLICANT: Wannemacher, Robert W  
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
 ; FILE REFERENCE: P67452US0 (RIID 01-58)  
 ; CURRENT APPLICATION NUMBER: US/10-083, 336A  
 ; CURRENT FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 11  
 ; LENGTH: 190  
 ; TYPE: PRT  
 ; ORGANISM: Ricinus communis  
 US-10-083-336A-11

Db 181 TRYNRS 190

RESULT 2  
US-10-083-336A-6  
Sequence 6, Application US/10083336A  
Publication No. US20030181665A1  
GENERAL INFORMATION:  
APPLICANT: Olson, Mark A  
APPLICANT: Millard, Charles B  
APPLICANT: Byrne, Michael P  
APPLICANT: Wannemacher, Robert W  
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
FILE REFERENCE: P67452US0 (RIID 01-58)  
CURRENT APPLICATION NUMBER: US/10/083,336A  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
TYPE: PRT  
ORGANISM: Ricinus communis

Query Match 99.6%; Score 971; DB 12; Length 189;  
Best Local Similarity 100.0%; Pred. No. 3.1e-103; Indels 0; Gaps 0;  
Matches 189; Conservative 0; Mismatches 0;

Qy 1 MIFPKQPIINFTAGATVQSYNTNFIRAVRGRLTIVLPNRVGLPINQRFLVLSNHAELS 60  
Db 1 MIFPKQPIINFTAGATVQSYNTNFIRAVRGRLTIVLPNRVGLPINQRFLVLSNHAELS 60  
Qy 61 VTLALDVTNAVYGYRAGNSAFFFPHQNQDAEATHLFTDVNRTFAFGNYDRLEQL 120  
Db 61 VTLALDVTNAVYGYRAGNSAFFFPHQNQDAEATHLFTDVNRTFAFGNYDRLEQL 120  
Qy 121 AGNLRENLGNGPЛЕAISALYYSTGGTQLPTLARSFICIQMISEAARFOYEGEMR 180  
Db 121 AGNLRENLGNGPЛЕAISALYYSTGGTQLPTLARSFICIQMISEAARFOYEGEMR 180  
Qy 181 TRYNRS 189  
Db 181 TRYNRS 189

RESULT 3  
US-10-083-336A-4  
Sequence 4, Application US/10083336A  
Publication No. US20030181665A1  
GENERAL INFORMATION:  
APPLICANT: Olson, Mark A  
APPLICANT: Millard, Charles B  
APPLICANT: Byrne, Michael P  
APPLICANT: Wannemacher, Robert W  
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
FILE REFERENCE: P67452US0 (RIID 01-58)  
CURRENT APPLICATION NUMBER: US/10/083,336A  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
TYPE: PRT  
ORGANISM: Ricinus communis

Query Match 99.1%; Score 966; DB 12; Length 188;  
Best Local Similarity 100.0%; Pred. No. 1.1e-102; Indels 0; Gaps 0;  
Matches 188; Conservative 0; Mismatches 0;

Qy 2 IFFPKQPIINFTAGATVQSYNTNFIRAVRGRLTIVLPNRVGLPINQRFLVLSNHAELS 61

RESULT 4  
US-10-083-336A-10  
Sequence 10, Application US/10083336A  
Publication No. US20030181665A1  
GENERAL INFORMATION:  
APPLICANT: Olson, Mark A  
APPLICANT: Millard, Charles B  
APPLICANT: Byrne, Michael P  
APPLICANT: Wannemacher, Robert W  
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
FILE REFERENCE: P67452US0 (RIID 01-8)  
CURRENT APPLICATION NUMBER: US/10/083,336A  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
TYPE: PRT  
ORGANISM: Ricinus communis

Query Match 98.5%; Score 960; DB 12; Length 200;  
Best Local Similarity 95.0%; Pred. No. 6.1e-102; Indels 0; Gaps 1;  
Matches 190; Conservative 0; Mismatches 0;

Qy 1 MIFPKQPIINFTAGATVQSYNTNFIRAVRGRLT-----VLPNRVGLPINQRFL 50  
Db 1 MIFPKQPIINFTAGATVQSYNTNFIRAVRGRLT-----VLPNRVGLPINQRFL 60

Qy 51 VELSNHAELSVTLAIDVDTNAVYGYRAGNSAYFFHDQDAEALTHLFTDVNRTFAF 110  
Db 61 VELSNHAELSVTLAIDVDTNAVYGYRAGNSAYFFHDQDAEALTHLFTDVNRTFAF 120

Qy 111 GGNYDRLEQLAGNTRENLGNGPЛЕAISALYYSTGGTQLPTLARSFICIQMISEA 170  
Db 121 GGNYDRLEQLAGNTRENLGNGPЛЕAISALYYSTGGTQLPTLARSFICIQMISEA 180

Qy 171 RFOYLEGEMTRIYNRSA 190  
Db 181 RFOYLEGEMTRIYNRSA 200

RESULT 5  
US-10-083-336A-8  
Sequence 8, Application US/10083336A  
Publication No. US20030181665A1  
GENERAL INFORMATION:  
APPLICANT: Olson, Mark A  
APPLICANT: Millard, Charles B  
APPLICANT: Byrne, Michael P  
APPLICANT: Wannemacher, Robert W  
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
FILE REFERENCE: P67452US0 (RIID 01-8)  
CURRENT APPLICATION NUMBER: US/10/083,336A  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
TYPE: PRT  
ORGANISM: Ricinus communis

Query Match 99.1%; Score 966; DB 12; Length 188;  
Best Local Similarity 100.0%; Pred. No. 1.1e-102; Indels 0; Gaps 0;

Qy

RESULT 6  
US-10-083-336A-5

Query Match      Best Local Similarity      Score      DB 12;      Length 188;  
Matches 186;      Conservative      0;      Mismatches 0;      Indels 0;      Gaps 0;

Qy      4 PQQYPIINFTAGATVQSYTNFTRAVGRGLTLPNRGLPINKQRFLIVELSNHAEISVTL 63  
Db      3 PQQYPIINFTAGATVQSYTNFTRAVGRGLTLPNRGLPINKQRFLIVELSNHAEISVTL 62

Qy      64 ALDVTNAYVGYRAGNSAYFFHDNOEAEATHLFIDVQNYTFAGFGNYDRLELAGN 123  
Db      63 ALDVTNAYVGYRAGNSAYFFHDNOEAEATHLFIDVQNYTFAGFGNYDRLELAGN 122

Qy      124 LRENIELGNGPLFEAISALYYSTGGTQLPTARSFLICIONISEARFOYIEGENRTRI 183  
Db      123 LRENIELGNGPLFEAISALYYSTGGTQLPTARSFLICIONISEARFOYIEGENRTRI 182

Qy      184 RYNRRS 189  
Db      183 RYNRRS 188

RESULT 6  
US-10-083-336A-5

Sequence 5, Application US/10083336A  
Publication No. US20030181665A1

GENERAL INFORMATION:

APPLICANT: Olson, Mark A  
APPLICANT: Millard, Charles B  
APPLICANT: Byrne, Michael P  
APPLICANT: Wannemacher, Robert W  
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
FILE REFERENCE: P67452050 (RIID 01-58)  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 15  
SEQUENCE DESCRIPTION: Patent in Ver. 2.1  
SEQ ID NO 5  
LENGTH: 199  
TYPE: PRT  
ORGANISM: Ricinus communis  
US-10-083-336A-5

Query Match      Best Local Similarity      Score      DB 12;      Length 199;  
Matches 189;      Conservative      0;      Mismatches 0;      Indels 10;      Gaps 1;

Qy      1 MFPKQPIINFTAGATVQSYTNFTRAVGRGLT-----VLPNRVSLPINORFIL 50  
Db      1 MFPKQPIINFTAGATVQSYTNFTRAVGRGLTGADRVRLITGADVRHEIPVNRYFIL 60

Qy      51 VLSNHAEISVTLADTVNAYVGYRAGNSAYFFHDNOEAEATHLFIDVQNYTFAF 110  
Db      61 VLSNHAEISVTLADTVNAYVGYRAGNSAYFFHDNOEAEATHLFIDVQNYTFAF 120

Qy      111 GNYDRLQLAGNLRENTELGNGPLEEAISALYYSTGGTQLPTARSFLICIONISEAA 170  
Db      121 GNYDRLQLAGNLRENTELGNGPLEEAISALYYSTGGTQLPTARSFLICIONISEAA 180

Qy      171 RFQYIEGMRTRIYRNRS 189  
Db      181 RFQYIEGMRTRIYRNRS 199

RESULT 7  
US-10-127-890-1

Sequence 1, Application US/10127890  
Publication No. US20030166196A1  
GENERAL INFORMATION:

RESULT 8

US-10-003-336A-1  
; Sequence 1, Application US/10083336A  
; Publication No. US20030181665A1  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Mark A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Byrne, Michael P  
; APPLICANT: Wannemacher, Robert W  
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
; CURRENT APPLICATION NUMBER: P67452US0 (RIID 01-58)  
; FILE REFERENCE: P67452US0 (RIID 01-58)  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 1  
; LENGTH: 576  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-003-336A-1

	Query Match	Score	DB	Length	Best Local Similarity	Pred.	No. Mismatches	Indels	Gaps
Qy	2 IFPKOPIINFTTAAATGATVQSYTNNFRAVRGRLT-----VLPNRVGLPINORFLY	97.9%	955;	576;	95.0%	1e-100;	0;	0;	
Ddb	36 IFPKOPIINFTTAAATGATVQSYTNNFRAVRGRLT-----VLPNRVGLPINORFLY	95							
Qy	52 ELSNHAELSVTLALDVTNAVVGTRAGNSAYFFHDQNDEAEAITHLFTDVQNRYTFAGF-----VLPNRVGLPINORFLY	96							
Ddb	96 ELSNHAELSVTLALDVTNAVVGTRAGNSAYFFHDQNDEAEAITHLFTDVQNRYTFAGF-----VLPNRVGLPINORFLY	15							
Qy	112 GNYDRLEQLAGNLRENTIELNGPRLRPAISALYYSTGGTOLPLARSFIIQMSSEAR-----VLPNRVGLPINORFLY	113							
Ddb	156 GNYDRLEQLAGNLRENTIELNGPRLRPAISALYYSTGGTOLPLARSFIIQMSSEAR-----VLPNRVGLPINORFLY	21							
Qy	172 FQYEGEMRTRIRYRNRRSA-----VLPNRVGLPINORFLY	190							
Ddb	216 FQYEGEMRTRIRYRNRRSA-----VLPNRVGLPINORFLY	234							

RESULT 9

US-10-003-336A-3  
; Sequence 3, Application US/10083336A  
; Publication No. US20030181665A1  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Mark A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Byrne, Michael P  
; APPLICANT: Wannemacher, Robert W  
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
; CURRENT APPLICATION NUMBER: P67452US0 (RIID 01-88)  
; FILE REFERENCE: P67452US0 (RIID 01-88)  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 3  
; LENGTH: 198  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-003-336A-3

	Query Match	Score	DB	Length	Best Local Similarity	Pred.	No. Mismatches	Indels	Gaps
Qy	2 IFPKOPIINFTTAAATGATVQSYTNNFRAVRGRLT-----VLPNRVGLPINORFLY	97.5%	951;	198;	94.9%	6.5e-101;	0;	0;	
Ddb	1 IFPKOPIINFTTAAATGATVQSYTNNFRAVRGRLT-----VLPNRVGLPINORFLY	51							
Qy	52 ELSNHAELSVTLALDVTNAVVGTRAGNSAYFFHDQNDEAEAITHLFTDVQNRYTFAGF-----VLPNRVGLPINORFLY	11							

Db	61	ELSNHAELSYTLAIDVITNAYTVGTYRAGNSAYFFHDQDAAEATHLFTDVQNRTYFAFG	120
Qy	112	GNYDRIEQLAGNLRENIELNGPLEEAISALYYSTGGTQLPTLARSFIICIQMISEAAR	171
Db	121	GNYDRIEQLAGNLRENIELNGPLEEAISALYYSTGGTQLPTLARSFIICIQMISEAAR	180
Qy	172	FQYIEGEMTRIYRNRS	189
Db	181	FQYIEGEMTRIYRNRS	198
<b>RESULT 10</b>			
	US-10-282-935-1		
;	Sequence 1, Application US/10282935		
;	Publication No. US20030143193A1		
;	GENERAL INFORMATION:		
;	APPLICANT: VITETTA, ELLEN S.		
;	GHETTE, VICTOR F.		
;	APPLICANT: SMALLISHAW, JOAN G.		
;	APPLICANT: BALUNA, ROXANA G.		
;	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF PROTEINACEOUS COMPOUNDS		
;	TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS		
;	CURRENT APPLICATION NUMBER: US/10/282,935		
;	CURRENT FILING DATE: 2002-10-29		
;	PRIOR APPLICATION NUMBER: 09/538,873		
;	PRIOR FILING DATE: 2000-03-30		
;	PRIOR APPLICATION NUMBER: 60/126,826		
;	PRIOR FILING DATE: 1999-03-30		
;	NUMBER OF SEQ ID NOS: 23		
;	FILE REFERENCE: USD-884US		
;	SEQ ID NO 1		
;	SOFTWARE: PatentIn Ver. 2.1		
;	TYPE: PRT		
;	ORGANISM: Artificial Sequence		
;	FEATURE:		
;	OTHER INFORMATION: Description of Artificial Sequence: Synthetic		
;	OTHER INFORMATION: Peptide		
US-10-282-935-1			
Query Match	96.9%	Score 945; DB 12; Length 267;	
Best Local Similarity	94.9%	Pred. No. 4.9e-100; Mismatches 0; Indels 10; Gaps 1;	
Matches	187;	Conservative 0; Mismatches 0; Indels 10; Gaps 1;	
Qy	4	PKQYPLINFTAGATVQSYTNFIRAVGRLT-----VLPNRVGLPINQRFLVEL	53
Db	3	PKQYPLINFTAGATVQSYTNFIRAVGRLTGADVRHETPVLPNRVGLPINQRFLVEL	62
Qy	54	SNHAELSYTLAIDVITNAYTVGTYRAGNSAYFFHDQDAAEATHLFTDVQNRTYFAFGN	113
Db	63	SNHAELSYTLAIDVITNAYTVGTYRAGNSAYFFHDQDAAEATHLFTDVQNRTYFAFGN	122
Qy	114	YDRLSQLAGNLRENIELNGPLEEAISALYYSTGGTQLPTLARSFIICIQMISAARFQ	173
Db	123	YDRLSQLAGNLRENIELNGPLEEAISALYYSTGGTQLPTLARSFIICIQMISAARFQ	182
Qy	174	YIEGEMTRIYRNRS	190
Db	183	YIEGEMTRIYRNRS	199
<b>RESULT 11</b>			
	US-10-440-796-1		
;	Sequence 1, Application US/10440796		
;	Publication No. US20040009148A1		
;	GENERAL INFORMATION:		
;	APPLICANT: VITETTA, ELLEN S.		
;	GHETTE, VICTOR F.		
;	APPLICANT: SMALLISHAW, JOAN G.		
;	APPLICANT: BALUNA, ROXANA G.		
;	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK SYNDROME (VLS)		
;	TITLE OF INVENTION: SYNTHETIC		

CURRENT APPLICATION NUMBER: US/10/440,796  
 CURRENT FILING DATE: 2003-05-19  
 PRIOR APPLICATION NUMBER: US/09/538,873  
 PRIOR FILING DATE: 2000-03-30  
 PRIOR APPLICATION NUMBER: 60/126,826  
 PRIOR FILING DATE: 1999-03-30  
 NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1  
 LENGTH: 267  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-10-440-796-1

Query Match 96.9%; Score 945; DB 12; Length 267;  
 Best Local Similarity 94.9%; Pred. No. 4.9e-100;  
 Matches 187; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy 4 PKQYPIINFTAGATVQSYTNFIRAVRGLT-----VLPRVGLPQNQRFLVEL 53  
 Db 3 PKQYPIINFTAGATVQSYTNFIRAVRGLTGADRVHEIPLVLPNVGLPQNQRFLVEL 62  
 Qy 54 SNAELSVTLALDVNAYVYGRAGNSAYFHPDNEQDAIAITHLFTDVQRYTFAFGGN 113  
 Db 63 SNAELSVTLALDVNAYVYGRAGNSAYFHPDNEQDAIAITHLFTDVQRYTFAFGGN 122  
 Qy 114 YDRLEQLAGNLRENTIELNGPLEEAISALYYSTGCGTQLPTLARSFIICIQMISEAARFQ 173  
 Db 123 YDRLEQLAGNLRENTIELNGPLEEAISALYYSTGCGTQLPTLARSFIICIQMISEAARFQ 182  
 Qy 174 YIEGMRTRIYNRRSA 190  
 Db 183 YIEGMRTRIYNRRSA 199

RESULT 12  
 US-10-083-336A-7  
 ; Sequence 7, Application US/1008336A  
 ; Publication No. US20030181665A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olson, Mark A  
 ; APPLICANT: Millard, Charles B  
 ; APPLICANT: Byrne, Michael P  
 ; APPLICANT: Wannemacher, Robert W  
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
 ; CURRENT APPLICATION NUMBER: US/10/083,336A  
 ; CURRENT FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 7  
 ; LENGTH: 198  
 ; TYPE: PRT  
 ; ORGANISM: Ricinus communis  
 US-10-083-336A-7

Query Match 96.5%; Score 941; DB 12; Length 198;  
 Best Local Similarity 94.9%; Pred. No. 9.2e-100;  
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy 4 PKQYPIINFTAGATVQSYTNFIRAVRGLT-----VLPRVGLPQNQRFLVEL 53  
 Db 3 PKQYPIINFTAGATVQSYTNFIRAVRGLTGADRVHEIPLVLPNVGLPQNQRFLVEL 62  
 Qy 54 SNAELSVTLALDVNAYVYGRAGNSAYFHPDNEQDAIAITHLFTDVQRYTFAFGGN 113  
 Db 63 SNAELSVTLALDVNAYVYGRAGNSAYFHPDNEQDAIAITHLFTDVQRYTFAFGGN 122  
 Qy 114 YDRLEQLAGNLRENTIELNGPLEEAISALYYSTGCGTQLPTLARSFIICIQMISEAARFQ 173

RESULT 13  
 US-10-083-336A-9  
 ; Sequence 9, Application US/1008336A  
 ; Publication No. US20030181665A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olson, Mark A  
 ; APPLICANT: Millard, Charles B  
 ; APPLICANT: Byrne, Michael P  
 ; APPLICANT: Wannemacher, Robert W  
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
 ; CURRENT APPLICATION NUMBER: US/10/083,336A  
 ; CURRENT FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 185  
 ; TYPE: PRT  
 ; ORGANISM: Ricinus communis  
 US-10-083-336A-9

Query Match 96.4%; Score 939.5; DB 12; Length 185;  
 Best Local Similarity 98.4%; Pred. No. 1.2e-99;  
 Matches 185; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 2 IFPQYPIINFTAGATVQSYTNFIRAVRGLTLPNRLPNQRFLVNRGLT---NRPGLPNQRFLVELSHAEHSV 61  
 Db 1 IFPQYPIINFTAGATVQSYTNFIRAVRGLTLPNRLPNQRFLVELSHAEHSV 57

Qy 62 TLALDVNAYVYGRAGNSAYFHPDNEQDAIAITHLFTDVQRYTFAFGNYTDRLEOLA 121  
 Db 58 TLALDVNAYVYGRAGNSAYFHPDNEQDAIAITHLFTDVQRYTFAFGNYTDRLEOLA 117  
 Qy 122 GNRLRENTIELNGPLEEAISALYYSTGCGTQLPTLARSFIICIQMISEAARFQTEGEERT 181  
 Db 118 GNRLRENTIELNGPLEEAISALYYSTGCGTQLPTLARSFIICIQMISEAARFQTEGEERT 177

Qy 182 RIRYRRSA 189  
 Db 178 RIRYRRSA 185

RESULT 14  
 US-10-083-336A-2  
 ; Sequence 2, Application US/1008336A  
 ; Publication No. US20030181665A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olson, Mark A  
 ; APPLICANT: Millard, Charles B  
 ; APPLICANT: Byrne, Michael P  
 ; APPLICANT: Wannemacher, Robert W  
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
 ; CURRENT APPLICATION NUMBER: P6742US0 (RIID 01-58)  
 ; CURRENT FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 179  
 ; TYPE: PRT  
 ; ORGANISM: Ricinus communis  
 US-10-083-336A-2

Query Match 69.6%; Score 679; DB 12; Length 179;  
 Best Local Similarity 93.1%; Pred. No. 9.9e-70;  
 Matches 134; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy            2 IFPKQYPIINFETTAGATVOSYTNTFIRAVGRLT-----VLPNRVLGINORFLY 51  
 Db            3 6 IFPKQYPIINFETTAGATVOSYTNTFIRAVGRLTGADYRHEIIVLPNRYGLP-INORFLV 95  
 Qy            52 ELSNHAEISVTIALDVTNAYVIGYRAGNSAYFFHPDNEQDAEARTHLEFTDVQNRYTAFG 111  
 Db            96 ELSNHAEISVTIALDVTNAYVIGYRAGNSAYFFHPDNEQDAEARTHLEFTDVQNRYTAFG 155  
 Qy            112 GNYDRLEQLAGNRENIELNGNGL 135  
 Db            156 GNYDRLEQLAGNRENIELNGNGL 179

---

RESULT 15  
 US-09-792-793A-39  
 Sequence 39; Application US/09792793A  
 Patent No. US2002018370A1  
 GENERAL INFORMATION  
 APPLICANT: McDonald, John R.  
 APPLICANT: Coggins, Phillip  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
 TITLE OF INVENTION: OTHER  
 FILE REFERENCE: 25020-601D  
 CURRENT APPLICATION NUMBER: US/09/792,793A  
 CURRENT FILING DATE: 2001-02-22  
 NUMBER OF SEQ ID NOS: 93  
 SEQ ID NO 39  
 SOFTWARE: PatentIn Ver. 2.0  
 LENGTH: 247  
 TYPE: PRT  
 ORGANISM: Trichosanthus kirilowii  
 US-09-792-793A-39

Query Match            34.5%; Score 336; DB 10; Length 247;  
 Best Local Similarity    38.9%; Pred. No. 3.9e-30;  
 Matches    72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;

Qy            10 INFPTAGATVOSYTNTFIRAVGRLTLPN-----RVGLPINORFLVLSNHAEL 59  
 Db            2 VSPRLSGATSSSYGVFSNLR--KALPNERKLYDIPRLSSLPGSORYALIHLINYADE 58  
 Qy            60 SYTFLADYTNAYVIGYRAGNSAYFFHPDNEQDA-EARTHLEFTDVQNRYTAFFGGNYDRLE 118  
 Db            59 TISVAIDTNTVIMGYRAGDSFF--NEASATEAKYVFDAMRKVTLPSGNTERLQ 115  
 Qy            119 QLAGNLENIELNGNGLPEEAISALYYXYSTGGTOLPLTARSFLICIQMISEARFOYTEGE 178  
 Db            116 TAGKIRENIPOLPALDSAITLFTYNAN---SAASALMVLQSTSEARRYKFIEQQ 170  
 Qy            179 MRTRI 183  
 Db            171 IGRV 175

Result No.	Score	Query Match Length	DB ID	Description
1	955	97.9	576	ricin D precursor - Tric agglutinin precursors
2	865.5	88.8	564	rRNA N-glycosidase abrin-d precursor
3	326	1	RLTAG	abrin-c precursor
4	327.5	33.6	289	abrin-d precursor
5	327.5	33.6	S32431	abrin-c precursor
6	326	33.4	562	Karasurin - Mongolic karasurin-B - Tric karasurin C - Tric abrin-b precursor
7	326	33.4	J00313	abrin (clone 7.2)
8	326	33.4	JC532	abrin-a precursor
9	323	33.1	JC5606	beta-luffin - smooth luffin b - smooth
10	310.5	31.8	S32430	rRNA N-glycosidase agglyutinin I precur-
11	303.5	31.1	C3761	rRNA N-glycosidase agglyutinin I precur-
12	300.5	30.8	S25260	rRNA N-glycosidase agglyutinin I precur-
13	294.5	30.1	T2USA	rRNA N-glycosidase agglyutinin I precur-
14	271.5	24.7	J00312	rRNA N-glycosidase agglyutinin I precur-
15	273	28.2	S2494	rRNA N-glycosidase agglyutinin I precur-
16	273	28.0	S28421	rRNA N-glycosidase agglyutinin I precur-
17	272	28.0	S26227	rRNA N-glycosidase agglyutinin I precur-
18	270	27.7	S2519	rRNA N-glycosidase agglyutinin I precur-
19	265	27.2	JC4840	rRNA N-glycosidase agglyutinin I precur-
20	264	27.1	J0018	mistletoe Lectin I
21	246.5	25.3	JT053	rRNA N-glycosidase agglyutinin I precur-
22	186.5	19.1	S28421	rRNA N-glycosidase agglyutinin I precur-
23	174	17.8	A39817	rRNA N-glycosidase agglyutinin I precur-
24	170	17.4	S17519	rRNA N-glycosidase agglyutinin I precur-
25	168.5	17.3	JE0401	antiviral protein
26	148.5	15.2	T1273	rRNA N-glycosidase agglyutinin I precur-
27	138	14.2	JC4811	betavulgin - beet rRNA N-glycosidase
28	131	13.4	S28542	agglyutinin I precur-
29	127	13.0	S28539	rRNA N-glycosidase

Post-processing: Maximum Match 100% Listing First 45 summaries				RESULT 1
Database : PIR_76:*				RICSD
1: Pir1:*				ricin D precursor - castor bean
2: Pir2:*				N; Contains: rRNA N-glycosidase (EC 3.2.2.22)
3: Pir3:*				C; Species: Ricinus communis (castor bean)
4: Pir4:*				C; Date: 31-Dec-1993 #sequence revision 16-Jul-1999
				C; Accession: A24041; S20513; A24614; A03374; A24010; S10303
				R; Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.P.
				Nucleic Acids Res. 13, 8019-8033, 1985
				A; Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
				A; Reference number: A24041; MUID: 8606724; PMID: 2999712
				A; Accession: A24041
				A; Molecule type: DNA
				A; Residues: 1-576 <TRE>
				A; Cross-references: EMBL:X52908; PID:CAA37095.1; PID:921085
				R; Lamb, P.J.; Roberts, L.M.
				Biochem. 148, 265-270, 1985
				A; Title: Nucleotide sequence of cloned cDNA coding for preproricin.
				A; Reference number: A24614; MUID: 85179479; PMID: 3838723
				A; Accession: A20513
				A; Molecule type: DNA
				A; Residues: 1-576 <TRE>
				A; Cross-references: GB:X03179; NID:921082; PID:921083
				R; Tregebar, J.W.; Roberts, L.M.
				Plant Mol. Biol. 18, 515-525, 1992
				A; Title: The lectin gene family of Ricinus communis: Cloning of a functional ricin gene c
				A; Reference number: S20513; MUID: 92163016; PMID: 1371405
				A; Accession: A24041
				A; Molecule type: DNA
				A; Residues: 1-576 <TRE>
				R; Lamb, P.J.; Roberts, L.M.; Jord, J.M.
				Biochem. 148, 265-270, 1985
				A; Title: Nucleotide sequence of cloned cDNA coding for preproricin.
				A; Reference number: A24614; MUID: 85179479; PMID: 3838723
				A; Accession: A20513
				A; Molecule type: mRNA
				A; Residues: 12-15, 'N'-77-550-'R'-552-576 <LAM>
				A; Cross-references: GB:X0388; NID:921078; PID:921085
				R; Yoshitake, S.; Funatsu, G.; Funatsu, M.
				Agriic. Biol. Chem. 42, 1267-1274, 1978
				R; Araki, T.; Funatsu, G.
				FEBS Lett. 191, 121-124, 1985
				A; Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan
				A; Reference number: A24010
				A; Molecule type: protein
				A; Residues: 36-97, 'Q'-99-109, 'S'-111-269, 'D'-272-283, 'L'-285-288, 'R'-290-302 <YOS>
				A; Note: this paper cites the others in the series providing experimental details for the
				R; Araki, T.; Funatsu, G.
				A; Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile che
				A; Reference number: A03372
				A; Molecule type: protein
				A; Residues: 36-97, 'Q'-99-109, 'S'-111-269, 'D'-272-283, 'L'-285-288, 'R'-290-302 <YOS>
				A; Note: this paper cites the others in the series providing experimental details for the
				R; Araki, T.; Funatsu, G.
				A; Title: Primary structure of Ala chain of ricin D.
				A; Reference number: A03374
				A; Molecule type: protein

## ALIGNMENTS

A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'E',402,'D',403,'B',404,'F',405-551,'V',553-527,E',529-564,'W',566,'H',567-570,L',573-574,F',<FUN>  
 A;Note: This paper, one of a series, summarizes the experimental details for the determination of the complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.  
 R;Ready, M.P.; Kim, Y.; Robertus, J.D.  
 Proteins 10, 220-278, 1991  
 A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of action. A;Contents: annotation; active site  
 R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.  
 Proteins 10, 251-255, 1991  
 A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.  
 A;Reference number: A48229; MUID:91352004; PMID:1881882  
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms  
 C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which inhibits protein synthesis; it inactivates the 60S ribosomal subunit of the cell of the A chain; B chains are also responsible for cell agglutination (lectin).  
 C;Comment: This protein is cytotoxic and very poisonous to animals.  
 C;Superfamily: ricin; rRNA N-glycosidase homology  
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed protein domain; ricin A-chain at 2.5 angstroms.  
 F;1-35/Domain: signal sequence #status predicted <SIG>  
 F;1-36/Domain: signal sequence #status predicted <ACH>  
 F;46-293/Domain: ricin D chain #status experimental <RNG>  
 F;315-576/Product: ricin D chain B #status experimental <BCH>  
 F;331-373,373-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats  
 F;45-409,449/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;115,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F;215/Active site: Glu #status experimental  
 F;294-318,334-333,377-394,465-478,514-521/Disulfide bonds: #status experimental  
 F;336,349,360/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status experimental  
 F;548,569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental

Query Match Score 97.9%; Best Local Similarity 95.0%; Length 576; Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Db 2 TRPKQYPTINFTAGATQYQSTNTNFIRAVRGRLT-----VLPNRVGLPINQRFLIV 51

Db 36 TRPKQYPTINFTAGATQYQSTNTNFIRAVRGRLT-----VLPNRVGLPINQRFLIV 95

Query Match Score 95.9%; Best Local Similarity 95.1%; Length 576; Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Db 2 TRPKQYPTINFTAGATQYQSTNTNFIRAVRGRLT-----VLPNRVGLPINQRFLIV 51

Db 36 TRPKQYPTINFTAGATQYQSTNTNFIRAVRGRLT-----VLPNRVGLPINQRFLIV 95

RESULT 3

Db 52 ELSNHAEILSVALTDVNAAYVGYRAGNSAYFFHPNQDEDAITHLFTDVQNYTFARG 111

Db 96 ELSNHAEILSVALTDVNAAYVGYRAGNSAYFFHPNQDEDAITHLFTDVQNYTFARG 155

Qy 112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGTQPLTLARSFIICLQMISEAR 171

Db 156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGTQPLTLARSFIICLQMISEAR 215

Qy 172 FOYIEGMRTRIYRNRSAA 190

Db 216 FOYIEGMRTRIYRNRSAA 234

Qy 52 ELSNHAEILSVALTDVNAAYVGYRAGNSAYFFHPNQDEDAITHLFTDVQNYTFARG 111

Db 96 ELSNHAEILSVALTDVNAAYVGYRAGNSAYFFHPNQDEDAITHLFTDVQNYTFARG 155

Qy 112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGTQPLTLARSFIICLQMISEAR 171

Db 156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGTQPLTLARSFIICLQMISEAR 215

Qy 172 FOYIEGMRTRIYRNRSAA 190

Db 216 FOYIEGMRTRIYRNRSAA 234

Qy 52 ELSNHAEILSVALTDVNAAYVGYRAGNSAYFFHPNQDEDAITHLFTDVQNYTFARG 111

Db 96 ELSNHAEILSVALTDVNAAYVGYRAGNSAYFFHPNQDEDAITHLFTDVQNYTFARG 155

Qy 112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGTQPLTLARSFIICLQMISEAR 171

Db 156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGTQPLTLARSFIICLQMISEAR 215

Qy 172 FOYIEGMRTRIYRNRSAA 190

Db 216 FOYIEGMRTRIYRNRSAA 234

Qy 52 ELSNHAEILSVALTDVNAAYVGYRAGNSAYFFHPNQDEDAITHLFTDVQNYTFARG 111

Db 96 ELSNHAEILSVALTDVNAAYVGYRAGNSAYFFHPNQDEDAITHLFTDVQNYTFARG 155

Qy 112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGTQPLTLARSFIICLQMISEAR 171

Db 156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGTQPLTLARSFIICLQMISEAR 215

Qy 172 FOYIEGMRTRIYRNRSAA 190

Db 216 FOYIEGMRTRIYRNRSAA 234

RESULT 2

RLCGAG agglutinin precursor - castor bean  
 N;Contains: rRNA N-Glycosidase (EC 3.2.2.22)  
 C;Species: Ricinus communis (castor bean)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999  
 R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.  
 R;Accession: A24261,A24210

J. Biol. Chem. 260, 15682-15686, 1985  
 A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.  
 A;Reference number: A24261; MUID:86059449; PMID:2993130

A;Accession: A24261  
 A;Molecule type: mRNA  
 A;Residues: 1-564 <ROB>  
 A;Cross-references: GB:ML2089; PID:9169700; PMID:AAA33869.1; PID:9169701

RLCSAG agglutinin precursor - castor bean  
 N;Contains: rRNA N-Glycosidase (EC 3.2.2.22)  
 C;Species: Ricinus communis (castor bean)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999  
 R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.  
 R;Accession: A24261,A24210

J. Biol. Chem. 260, 15682-15686, 1985  
 A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.  
 A;Reference number: A24261; MUID:86059449; PMID:2993130

A;Accession: A24261  
 A;Molecule type: mRNA  
 A;Residues: 1-564 <ROB>  
 A;Cross-references: GB:ML2089; PID:9169700; PMID:AAA33869.1; PID:9169701

R;Araki, T.; Yoshioka, Y.; Funatsu, G.; Biochim. Biophys. Acta 872, 277-285, 1986  
 A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.  
 A;Reference number: A24210  
 A;Accession: A24210

A;Molecule type: Protein  
 A;Residues: 303-325,'F',327-330,'T',332-361,'D',363-373,'G',375-403,'T',405-551,'V',553-527,C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared to ricin; rRNA N-glycosidase homology  
 C;Superfamily: ricin; rRNA N-glycosidase homology  
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed; F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;35-281/Domain: rRNA N-glycosidase homology  
 F;303-564/Product: agglutinin chain B #status experimental <BCH>  
 F;319-361,362-402,405-443,448-528,529-567/Region: 40-residue repeats  
 F;34-259/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F;200,203/Active site: Glu, Arg #status predicted  
 F;282-306,322-341,365-382,451-466,492-509/Disulfide bonds: #status predicted  
 F;324,337,348/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status predicted  
 F;536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted  
 Query Match Score 88.8%; Best Local Similarity 86.9%; Length 564; Matches 173; Conserv. 7; Mismatches 8; Indels 11; Gaps 2;

Qy 2 IFPKQYPTINFTAGATQYQSTNTNFIRAVRGRLT-----VLPNRVGLPINQRFLIV 51

Db 25 IFPKQYPTINFTAGATQYQSTNTNFIRAVRGRLT-----VLPNRVGLPINQRFLIV 84

Qy 52 ELSNHAEILSVALTDVNAAYVGYRAGNSAYFFHPNQDEDAITHLFTDVQNYTFARG 111

Db 85 ELSNHAEILSVALTDVNAAYVGYRAGNSAYFFHPNQDEDAITHLFTDVQNSTFARG 144

Qy 112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGTQPLTLARSFIICLQMISEAR 171

Db 145 GNYDRLEQ-LGGLRNLTEGTGLEDAISALYYYSTGTQPLTLARSFIICLQMISEAR 203

Qy 172 FOYIEGMRTRIYRNRSAA 190

Db 204 FOYIEGMRTRIYRNRSAA 222

RTLTZ

N;Alternate names: alpha-TCS; type I ribosome-inactivating protein - Mongolian snake-gourd  
 C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)  
 C;Date: 30-Sep-1988 #sequence\_revision 26-Jan-1986 #text\_change 23-Mar-2001  
 C;Accession: JT0066; A36274; JC103; A36273; JT0003  
 R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.  
 Gene 97, 267-272, 1991  
 A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.  
 A;References number: JT0566; MUID:91153657; PMID:199231  
 A;Accession: JT0566  
 A;Molecule type: mRNA  
 A;Residues: 1-289 <SHA>  
 A;Cross-references: GB:M34858; PID:9170536; PMID:AAA34207.1; PID:9170537  
 A;Experimental source: tuber  
 R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.  
 J. Biol. Chem. 265, 8670-8674, 1990  
 A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribonuclease  
 A;Reference number: A36274; MUID:90256790; PMID:2341400  
 A;Accession: A36274  
 A;Molecule type: DNA  
 A;Residues: 1-233,'T',225-246,'M',248-289,<CHO>  
 A;Cross-references: GB:M105434; PID:9170534  
 R;Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.  
 Acta Genet. Sin. 21, 42-51, 1994  
 A;Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.  
 A;Reference number: JC1093; MUID:94271613; PMID:8003348  
 A;Accession: JC1093

C;Species: Abrus precatorius (Indian licorice) C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997	
C;Accession: S34408 ; S34408 R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y. J.J. Mol. Biol. 229, 263-267, 1993	
A;Title: Primary structure of three distinct isoabutins determined by cDNA sequencing. Correlation to the EMBL Data Library, March 1993	
A;Reference number: S32429; MUID:93132798; PMID:8421313 A;Accession: S34408 A;Molecule type: mRNA A;Residues: 1-528 <HUN>	
A;Cross-references: GB:M98346 A;Cross-references: GB:M98346	
C;Comment: Abutin consists of an A chain, which inhibits protein synthesis by inactivating The A and B chains are linked by a single disulfide bond, which is essential for toxicit C;Keywords: ricin: rRNA N-glycosidase homology C;Keywords: disulfide bond: duplication; glycoprotein; glycosidase; hydrolase; lectin; pI: 7.251/Product: abrin-d chain A #status predicted <ACH> F:7-2467/Domain: rRNA N-glycosidase homology <RNG> F:261-528/Product: abrin-d chain B #status predicted <BCH> F:28-325/326-366,139-407,414-449,453-492,95-528/Region: 40-residue repeats F:1/Modified site: Pyrrolidone carboxylic acid (Gln) #status predicted F:164,167/Active site: substrate (Tyr, Tyr, Glu, Asn) #status predicted F:200,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted F:113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted F:286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted F:288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted F:500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted	
Query Match Best Local Similarity 33.6%; Score 327.5; DB 2; Length 528; Matches 82; Conservative 22; Mismatches 68; Indels 15; Gaps 4;	
Qy 6 QYPLINFTAGATVQSYTNFIRAVGRLLT-----VLPNVRVGLPINORFILVLSNHA 57 Ddb 1 QDQYIKFTTEGATQSQYKQFIEALQRQLTGGLIHDIPVLDPTIVERNRYITVLSNSE 60	
Qy 58 ELSVTYLLADTYNAVYYGYTRAGNSAYFHDNOEADAIFHLFTDVQNRYTFAGGNYDRL 117 Ddb 61 RESIEGVIDDTVNAVVAATRAGSQSYFL--RDADASASTYLEPCTQ--RVSRLRFDSYGDQ 116	
Qy 118 EQLAGNLRNTRNIELGNGPLEBAISLYYKSTGGTQLPLTARSFLICIQMISBAARPQYIEG 177 Ddb 117 ERWAHQTRBEISLQLQTHAIS---FLRGASNDERKTLIVIVQMSEAARYIYSEN 173	
Qy 178 EMTRTR 184 Ddb 174 RGVYSIR 180	
RESULT 5 S16022 abrin-c precursor - Indian licorice A;Contains: rRNA N-glycosidase (EC 3.2.2.22) C;Species: Abrus precatorius (Indian licorice) C;Accession: S16022 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999 Eur. J. Biochem. 198, 723-732, 1991 A;Title: Preabrin: Genomic cloning, characterisation and the expression of the A-chair A;Reference number: S16022; MUID:91266957; PMID:2050149 A;Accession: S16022 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-562 <WOO> A;Cross-references: ENBL:X55667; NID:916084; PID:CAA39202.1; PID:gi16085 C;Comment: Abutin consists of an A chain, which inhibits protein synthesis by inactivating The A and B chains are linked by a single disulfide bond, which is essential for toxicit	

C;Superfamily: ricin; rRNA N-glycosidase homology  
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid  
 F:41\_280/Domain: rRNA N-glycosidase homology <RNG>  
 F:29\_562/Product: abrin-c chain B #status Predicted <ACH>  
 F:29\_562/Domain: rRNA N-glycosidase homology <RNG>  
 F:31\_395\_360\_403\_448\_483\_487\_516\_539\_562/Region: 40-residue repeats  
 F:35/Modified site: Pyrrolidine carbonylic acid (Gln) (in mature form) #status Predicted  
 F:108\_147\_229\_230/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status Predicted  
 F:23\_287\_395\_435\_436/Binding site: carboxylic (Asn) (covalent) #status Predicted  
 F:281\_320\_320\_339\_363\_380\_451\_464\_490\_507/Bisulfide bonds: #status Predicted  
 F:32\_346\_346/Binding site: N-acetylgalactosamine (Asp, Asn) #status Predicted  
 F:53\_555\_555/Binding site: N-acetylgalactosamine (Asp, Asn) #status Predicted

Query Match Score 327.5%; Score 327.5%; Score 327.5%;  
 Best Local Similarity 43.9%; Fred. No. 3.9e-22; Mismatches 22; Indels 15; Gaps 4;  
 Matches 82; Conservative 82; Mismatches 68; Indels 15; Gaps 4;

Qy 6 QPYINNETTAGATQSYTNFIRAVRGLT-----VLENRVLGLPINQRFLIVELSNHA 57  
 Db 35 QDQVKTFFETCATSSYKQFENQLRITIPDPTIVEERNYITVELNSNE 94  
 Qy 58 ELSVTIALDVNTAYVGYRAGNSAYFFHDNQEDAIAITHLFTDQNRTFAFGNNYDRL 117  
 Db 95 RESIEVGIDNTAYVGYRAGNSQYFL--RDAPASASTYFFGQI-RYSLRFDSYGD 150  
 Qy 118 EQLAGNIRENTLENGNPLEAISALYYSTGGTQPLTLLARSEFIQJOMISEAARQYIEG 177  
 Db 151 ERWAHQTRTEESLGLQALTHAIS--FLRSGASNDEEKARTLIVIOMASEAARYRYISN 207  
 Qy 178 EMRTRIR 184  
 Db 208 RGVNSTR 214  
 Qy 182 RI 183  
 Db 174 RV 175

## RESULT 6

JU0393 karausurin - Mongolian snake-gourd (Mongolian snake-gourd)  
 C;Species: Trichosanthes kirilowii var. japonica  
 C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 12-Apr-1995  
 R;Toyonaka, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.  
 A;Title: The complete amino acid sequence of an abortifacient protein, karausurin.  
 A;Reference number: JU0393; PMID:19140000  
 A;Accession: JU0393  
 A;Molecule type: protein  
 A;Residues: 1-247 <TOY>  
 A;Note: a sequence which lacks Ala-247 is also shown in this publication  
 C;Keywords: rRNA N-glycosidase; rRNA N-glycosidase homology  
 F:4\_243/Domain: rRNA N-glycosidase homology <RNG>

Query Match Score 326%; Score 326%; Score 326%;  
 Best Local Similarity 39.6%; Fred. No. 1.9e-22; Mismatches 44; Indels 16; Gaps 5;  
 Matches 72; Conservative 72; Mismatches 50; Indels 16; Gaps 5;

Qy 10 INFITAGATQSYTNFIRAVR-----GRUTVLP-NRUGLPIINQRFLIVELSNHAELSVT 62  
 Db 2 VSFRUSGATSSSYGVTSNRKALPYERKLYDIPLRSTLPGSQRYALJHLTNADETIS 61  
 Qy 63 LALDVNTAYVGYRAGNSAYFFHDNQEDA-EAITHLFTDQNRTFAFGNNYDRLEQLA 121  
 Db 62 VAIDVNTYVGYRAGDSYFF--NEASATEAAKYVKDAREKVTLPSGNYERLQJAA 118  
 Qy 122 GNRLRNIELGNGPLEAISALYYSTGGTQPLTLLARSEFIQJOMISEAARQYIEGMR 181  
 Db 119 GKIRENIPGLPALSATTTFLYNNAN---SAASALMVLQSTSEARRYKFLEQQIGK 173  
 Qy 182 RI 183  
 Db 174 RV 175

## RESULT 8

JC5606 karausurin C - Trichosanthes kirilowii var. japonica  
 N;Contains: karausurin A  
 C;Species: Trichosanthes kirilowii var. japonica  
 C;Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 19-Jul-2002  
 R;Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.  
 A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating protein  
 A;Reference number: JC5606; PMID:97316562; PMID:9212998  
 A;Accession: JC5606  
 A;Molecule type: DNA  
 A;Residues: 1-289 <MIIZ>  
 A;Cross-references: DDBJ:AB000666; NID:G2329830; PTDN:BAA21786.1; PID:92329831  
 R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.  
 A;Biol. Pharm. Bull. 19, 1485-1489, 1996  
 A;Title: Amino acid sequences and ribosome-inactivating activities of karausurin-B and ka:  
 A;Accession: JC5033  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 22-270 <KOR>  
 C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalytic  
 C;Superfamily: rRNA N-Glycosidase; rRNA N-glycosidase homology  
 F:22\_270/Product: karausurin C #status predicted <MAC>  
 F:24\_270/Product: karausurin A #status predicted <MAC>  
 F:27\_266/Domain: rRNA N-glycosidase homology <RNG>

Query Match Score 33.4%; Score 326%; DB 2; Length 247;  
 Best Local Similarity 39.6%; Pred. No. 2.e-22; Mismatches 44; Indels 16; Gaps 5;  
 Matches 72; Conservative 72; Mismatches 50; Indels 16; Gaps 5;

Qy 122 GNRLRNIELGNGPLEAISALYYSTGGTQPLTLLARSEFIQJOMISEAARQYIEGMR 181  
 Db 119 GKIRENIPGLPALSATTTFLYNNAN---SAASALMVLQSTSEARRYKFLEQQIGK 173  
 Qy 182 RI 183  
 Db 174 RV 175



A;Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein  
A;Reference number: JT0202  
A;Molecule type: protein  
A;Residues: 1-201; 203-251 <FUN>  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
R;Evensen, G.; Mathiesen, A.; Sundan, A.  
J. Biol. Chem. 266, 6848-6852, 1991  
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.  
A;Reference number: A39761; MUID:91201329; PMID:2016300  
A;Status: nuclease sequence not shown  
A;Molecule type: DNA  
A;Residues: 'E', 2-251 <EV>  
A;Cross-references: GB:X54972  
A;Note: residues 1-8 were derived from the synthesized primer  
R;Kimura, M.; Sunizawa, T.; Funatsu, G.  
Biotech. Biotechnol. Biochem. 57, 156-169, 1993  
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic  
A;Reference number: JCL398; MUID:93169023; PMID:7763422  
A;Comments: seeds  
A;Accession: JC1398  
A;Molecule type: protein  
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>  
A;Experimental source: seed  
R;Evensen, G.; Mathiesen, A.; Sundan, A.  
Submited to the EMBL Data Library, October 1990  
A;Description: Direct molecular cloning of two distinct abrin A-chains.  
A;Reference number: S14471  
A;Accession: S14472  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 'ME', 2-251 <EV>  
A;Cross-references: EMBL:X54873; NID:916090; PIDN:CAA38655.1; PID:916091  
R;Chen, Y.L.; Chow, L.P.; Tsugita, A.; Lin, J.Y.  
FEBS Lett. 309, 115-118, 1992  
A;Title: The complete primary structure of abrin-a B chain.  
A;Reference number: S24133; MUID:92371656; PMID:1505674  
A;Accession: S24133  
A;Molecule type: protein  
A;Residues: 262-297, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 <CHE>  
R;Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.  
Eur. J. Biochem. 240, 564-569, 1996  
A;Title: Probing the domain structure of abrin-a by tryptic digestion.  
A;Reference number: S74110; MUID:97008945; PMID:8896055  
A;Accession: S74110  
A;Molecule type: protein  
A;Residues: 89-108; 154-172 <LIN>  
A;Experimental source: seed  
A;Accession: S74111  
A;Molecule type: protein  
A;Experimental source: seed  
C;Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which contains receptors on the cell surface. The A and B chains are linked by a single disulfide bond.  
C;Superfamily: ricin; rRNA N-glycosidase homology  
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid  
F;1-251; Product: abrin-a chain A #status experimental <ACH>  
F;7-246; Domain: rRNA N-glycosidase homology <RNG>  
F;261-328; Product: abrin-a chain B #status experimental <BCH>  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;74,113,195,196; Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F;14,167,169,206-305,329-346,417-430,455-473; Disulfide bonds: #status predicted  
F;288,312; Binding site: N-acetyl galactosamine (Asp, Asn) #status predicted  
F;361,401; Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;500,521; Binding site: N-acetyl galactosamine (Asp, Asn) #status predicted

Qy 10 INFTTAGATVOSYTINFRAYVRGRL-----TVLPNRVGLPINORFLVELSNHAEISV 61  
Db 5 IKFSTEGATSSOSYKOFIEARLERLRRGLIDIPVLPDTIQLERNRYITELNSNTDESI 64  
Qy 62 TLALDVTNAVVGPRAGNSAYFFH - PDNGDDEAITHLTFDQNRTYFAFGGNYDRLEQ 119  
Db 65 EVGIDVTNAVVAVYRAGTOSYFLRDAPSSASD----SYLFGTG-DQHSLPFYGTGDLER 118  
Qy 120 LAGNRENIIEGNGPEEAISALYYSTSGTQQLPLARSFLICOMISEEARFOYIEGEM 179  
Db 119 WAHQSRQIPIGLQRLTHGIS---FRRSGENDNEEKARTLIVIOMAEEARFRYNSRV 175  
Qy 180 RTRIR 184  
Db 176 RVSIQ 180

RESULT 12  
S23519  
C;Species: *Luffa cylindrica* (smooth loofah)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 20-Aug-1999  
C;Accession: S23519; S23113  
R;Kacaka, J.; Habuka, N.; Miyano, M.; Matsuta, C.; Koiwai, A.  
Plant Mol. Biol. 19, 887-889, 1992  
A;Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating  
A;Reference number: S23519; MUID:92353400; PMID:1642320  
A;Accession: S23519  
A;Cross-references: EMBL:X62372; NID:919149; PIDN:CAA44230.1; PID:919150  
A;Raidius: 1-278 <CAT>  
A;Molecule type: mRNA  
C;Superfamily: rRNA N-glycosidase homology  
F;26-264; Domain: rRNA N-glycosidase homology <RNG>  
Query Match 30-8%; Score 300.5; DB 2; Length 278;  
Best Local Similarity 35.3%; Pred. No. 4 7e-20;  
Matches 66; Conservative 43; Mismatches 57; Indels 21; Gaps 4;

Qy 10 INFTTAGATVOSYTINFRAYVRGRL-----TVLPNRVGLPINORFLVELSNHAEISV 59  
Db 24 VSFSLSGADSRSKSYSKEITAIRKALPSKEVKVSNIPLPSASGA---SRYTMLQNSYDAK 80  
Qy 60 SVTLADVTNAVVGPRAGNSAYFFHPDNGDDEAITHLTFDQNRTYFAFGGNYDRLEQ 119  
Db 81 AITMADVTNYTIMGVLNTNSYFF--NESDAKLASQYFKGSITVLYPSGYNERLQN 137  
Qy 120 LAGNRENIIEGNGPEEAISALYYSTSGTQQLPLARSFLICOMISEEARFOYIEGEM 179  
Db 138 AAGKVREKIPLGRAFDSAITSLHYD---TAAGAFLVIIQTAAERSRKYIEGQI 192  
Qy 180 RTRIRYN 186  
Db 193 TERIPRN 199

RESULT 13  
JN0108  
Luffin-b - smooth loofah  
C;Species: *Luffa cylindrica* (smooth loofah)  
C;Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 07-May-1999  
C;Accession: JN0108  
R;Islam, M.R.; Hirayama, H.; Funatsu, G.  
Agric. Biol. Chem. 55, 229-238, 1991  
A;Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from  
A;Reference number: JN0108; MUID:91248488; PMID:1368666  
A;Accession: JN0108  
A;Status: Preliminary  
A;Molecule type: protein  
A;Residues 1-250 <SL>  
C;Superfamily: rRNA N-glycosidase homology  
F;5-246; Domain: rRNA N-glycosidase homology <RNG>  
Query Match 30.1%; Score 293.5; DB 2; Length 250;

Best Local Similarity 33.7%; Pred. No. 1.8e-19; Matches 63; Conservative 46; Mismatches 57; Indels 21; Gaps 4;

Qy 10 INFETTAGATVQSYTNEFIRAVGRRL-----TVLPNRYGLPINORFLIVELSNHAEI 59  
Db 3 VFSLSGADSKSYKSKFTALRAPSKEVKNSNPLILPSASSA---SRYTLMQLSNYDAK 59

Qy 60 SUTLALLYNTNATVGRAGNSYFFHPDNQEAEATHLFITVQNRVTFARGGNYDLEQ 119  
Db 60 ALTMADTVNTVYNGLYVNNTSYF---ANESAKLASOQYVFKGSTLVTFSGNTVERLQN 116

Qy 120 IAGNLNRTENITLGNGPLEIAISALYYSTGGTOLPFLARSTFCITOMISEAARFOYIEGEM 179  
Db 117 AGKIKRKEIPLOFRAIDSALTSIFHYDS---TAAAAFLVILQTTAEASRFKTEGQI 171

Qy 180 RTRIYN 186  
Db 172 IERIPKN 178

RESULT 14

S22494 rRNA N-glycosidase (EC 3.2.2.22) alpha-luffin precursor - smooth loafah  
;rRNA N-glycosidase (EC 3.2.2.22) alpha-luffin precursor - smooth loafah  
;N;Alternate names: agglutinin; momordica charantia; ribosome-inactivating protein momorcharin alpha  
;C;Species: Luffa cylindrica (smooth loafah)  
;C;Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text\_change 20-Aug-1999  
;C;Accession: S22494; S26330; JF0202; A32342  
;R;Katohka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.  
;A;Title: Complete amino acid sequence of cDNA encoding alpha-luffin, a ribosome-inactivating protein from Luffa cylindrica. Plant Mol. Biol. 18, 1199-1202, 1992  
;A;Reference number: S22494; MUID:92288316; PMID:1600156  
;A;Molecule type: tRNA  
;A;Residues: 1-27 <RAT>  
;A;Cross-references: EMBL:X62371; PIDN:919145; PIDN:CAA44229.1; PID:919146  
;R;Islam, M.R.; Nishida, H.; Funatsu, G.  
;A;Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from Luffa cylindrica. Agric. Biol. Chem. 54, 2967-2978, 1990  
;A;Reference number: S26390; MUID:91248471; PMID:1368651  
;A;Accession: S26390  
;A;Molecule type: protein  
;A;Residues: 21-33,'L',55,'I',57-86,'SQL',90-154,'L',156-157,'I',159-173,'L',175-209,'SL'  
;R;Islam, M.R.; Nishida, H.; Funatsu, G.  
;A;Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from Luffa cylindrica. Agric. Biol. Chem. 54, 133-1345, 1990  
;A;Reference number: JH0202; MUID:91197482; PMID:91197482  
;A;Molecule type: protein  
;A;Residues: 21-55,'L',55,'I',57-86,'SQL',90-154,'L',156-157,'I',159-173,'L',175-209,'SL'  
;A;Experimental source: seed  
;R;Ramakrishnan, S.; Engblom, J.-J.; Bryant Jr., H.L.; Xu, F.J.  
;A;Characterization of a translation inhibitory protein from Luffa aegyptiaca. Biochem. Biophys. Res. Commun. 160, 509-516, 1989  
;A;Reference number: A32542; MUID:89246493; PMID:2719679  
;A;Accession: A32542  
;A;Status: preliminary  
;A;Molecule type: protein  
;A;Residues: 21-29,'G',30,'X',32-34,'K',36-40 <RAM>  
;C;Function:  
;A;Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA ther

Best Local Similarity 33.3%; Pred. No. 1.1e-17; Mismatches 42; Indels 23; Gaps 5;

Query Match 28.2%; Score 274.5; DB 2; Length 277;  
Best Local Similarity 33.3%; Pred. No. 1.1e-17; Mismatches 42; Indels 23; Gaps 5;

F;24-269/Producent: rRNA N-glycosidase alpha-momorcharin #status experimental <MAT>  
 F;27-266/Domain: rRNA N-glycosidase homology <RNC>  
 F;27-286/Domain: carboxyl-terminal propeptide #status predicted <CPB>  
 F;93-183-186/Active site: Tyr, Glu, Arg #status predicted  
 F;250/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match	28.0%	Score 273;	DB 1;	Length 286;
Best Local Similarity	34.8%	Pred. No. 1.6e-17;		
Matches	63;	Conservative	Mismatches 40;	Indels 16;
				Gaps 4;

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Qy      10 INFPTAGATVOSYTINPIRAVGRILTVLPNRVLPLI-----NQRFILVELSNHAELSVT 62
Db      25 VSFRISGADPSYGMETIKDRLNALPFPREKYNIPNILLPSVSGAFLMMLFENDGKTIT 84
Qy      63 IALDVTNAIVVGYGRNSAIFHPQNQEDAE-AIHLFDWQNRHTFAGGNYDLEQLA 121
Db      85 VADVTNNVYIMGYLADTTSFV---NEPAEALASQYVFRARRKTLPSGGNYERLQAA 141
Qy      122 GNLRENTIELNGNPLEFAISALLYYSTGGTQOPTLARSFLICIQTMISEAARFOYIEGEMET 181
Db      142 GKPREKPIGLPALDSAIStLRYDS----TAAAGALLVLIQTAEARFKYIEQQIDE 196
Qy      182 R 182
Db      197 R 197

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Search completed: February 10, 2004, 16:28:04  
 Job time : 11.2817 secs





Query Match Score 955; DB 1; Length 576;  
 Best Local Similarity 95.0%; P.ref. No. 1; Seq. 81; Mismatches 0; Indels 10; Gaps 1;  
 Matches 189; Conservative 0;

Qy 2 IFPKQYPIINFTAGATQSYNTNFIRAVRGRFT-----VLDNRYGLFINQRFILV 51  
 Db 36 IFPKQYPIINFTAGATQSYNTNFIRAVRGRFT-----VLPNVRGLFINQRFILV 95

Qy 52 ELSNHAELSVTALDVNTAYVGYRAGNSAYFHPDNEQDAIAITHLFTDVNRYTFAGF 111  
 Db 96 ELSNHAELSVTALDVNTAYVGYRAGNSAYFHPDNEQDAIAITHLFTDVNRYTFAGF 155

Qy 112 GNYDRLEQLAGNLRENTLGNGPLEEATSLAYYYSTGQLPTLARSFIICIQMISEAAR 171  
 Db 156 GNYDRLEQLAGNLRENTLGNGPLEEATSLAYYYSTGQLPTLARSFIICIQMISEAAR 215

Qy 172 FOYIEGEMRTRTRYNRRSA 190  
 Db 216 FOYIEGEMRTRTRYNRRSA 234

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RESULT 2

AGGL_RICCO	STANDARD;	PRT;	564 AA.
ID	AGGL_RICCO		
AC	P06750;		
DT	01-JAN-1988 (Rel. 06, Created)		
DT	01-JAN-1988 (Rel. 06, Last sequence update)		
DE	Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-sugcosidase) (EC 3.2.2.22); Agglutinin B chain].		
DE	Ricinus communis (Castor bean)		
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophita; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Ericoids 1; Malpighiales; Euphorbiaceae; Ricinus.		
RN	SEQUENCE FROM N.A. MEDLINE=86509449; PubMed=2999120; Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.: "The primary sequence of Ricinus communis agglutinin. Comparison with ricin." RT "The primary sequence of Ricins communis agglutinin. Comparison with ricin." RT ricin."		
RL	J. Biol. Chem. 260:15682-15686(1985). RT SEQUENCE OF 303-564.		
RP	SEQUENCE OF 303-564.		
RC	TISSUE=Seed.		
RA	"Araki T.", Yoshida Y., Funatsu G.; "The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds." RT Biochim. Biophys. Acta 872:277-285(1986). IZ]		
RA	Medline=80178723; PubMed=6768555; Lin T.T.-S., Li S.-L.; "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis." RT Eur. J. Biochem. 105:453-459 (1980).		
CC	-- CATALYTIC ACTIVITY: Endohydrolase of the N-Glycosidic bond at one specific adenosine on the 28S rRNA.		
CC	-- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.		
CC	-- SIMILARITY: Contains 2 ricin B-type lectin domains.		
CC	This SWISS-PROT entry is copyright produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).		
CC	DR M1089; AAA33869.1; "Ribosome-inactivating protein alpha-trichosanthin precursor (rrNA N-Glycosidase) (EC 3.2.2.22) (Alpha-TCS)." EMBL; S40368; ARB22584.1; "		

DR PIR; A24261; RICSAQ.  
 DR HSSP; P02879; 1BR6.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 SMART; SM00458; RICIN; 2.  
 DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.

POTENTIAL,  
 AGGLUTININ A CHAIN.  
 LINKER PEPTIDE.

FT SIGNAL 1 24  
 FT CHAIN 25 290  
 FT PROPEP 291 302  
 FT CHAIN 303 564  
 FT DOMAIN 309 436  
 FT DOMAIN 439 563  
 FT REPEAT 319 361  
 FT REPEAT 362 402  
 FT REPEAT 405 437  
 FT REPEAT 450 485  
 FT REPEAT 489 528  
 FT REPEAT 531 558  
 FT ACT SITE 200 200  
 FT DISULFID 282 306  
 FT DISULFID 322 341  
 FT DISULFID 365 382  
 FT DISULFID 453 466  
 FT DISULFID 492 509  
 FT CARBOHYD 34 34  
 FT CARBOHYD 259 259  
 FT CARBOHYD 397 397  
 FT CARBOHYD 437 437  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 331 331  
 FT CONFLICT 362 362  
 FT CONFLICT 374 374  
 FT CONFLICT 404 404  
 PT CONFLICT 552 552  
 SQ SEQUENCE 564 AA; 62851 MW; D455F2A7F609759 CRC64;

Query Match Score 865.5; DB 1; Length 564;  
 Best Local Similarity 86.9%; Pred. No. 3.3e-73; Matches 173; Conservative 7; Mismatches 8; Indels 11; Gaps 2;

Qy 2 IFPKQYPIINFTAGATQSYNTNFIRAVRGRFT-----VLPNVRGLFINQRFILV 51  
 Db 25 IFPKQYPIINFTAGATQSYNTNFIRAVRGRFT-----VLPNVRGLFINQRFILV 84

Qy 52 ELSNHAELSVTALDVNTAYVGYRAGNSAYFFHPDNEQDAEAITHLFTDVNRYTFAGF 111  
 Db 85 ELSNHAELSVTALDVNTAYVGYRAGNSAYFFHPDNEQDAEAITHLFTDVNRYTFAGF 144

Qy 112 GNYDRLEQLAGNLRENTLGNGPLEEATSLAYYYSTGQLPTLARSFIICIQMISEAAR 171  
 Db 145 GNYDRLEQ-LGRLRENTLGNGPLEDAISAYYYTCGTQPLTARSFIICIQMISEAAR 203

Qy 172 FOYIEGEMRTRTRYNRRSA 190  
 Db 204 FOYIEGEMRTRTRYNRRSA 222

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RESULT 3

RIP_TRIKI	STANDARD;	PRT;	289 AA.
ID	RIPT_TRIKI		
AC	P09989;		
DT	01-MAR-1989 (Rel. 10, Created)		
DT	01-NOV-1990 (Rel. 16, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DB	Ribosome-inactivating protein alpha-trichosanthin precursor (rrNA N-Glycosidase) (EC 3.2.2.22) (Alpha-TCS).		
OS	Trichosanthes kirilowii (Mongolian snake-gourd).		

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OX eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.

[1] — SEQUENCE FROM N.A.  
 RN STRAIN=Maximowicz;  
 RC MEDLINE=91153657; PubMed=1999291;  
 RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;  
 RT "Cloning of trichosanthin cDNA and its expression in Escherichia  
 coli";  
 RT Gene 97:267-272 (1991).

[2] — SEQUENCE FROM N.A.  
 RC STRAIN=Maximowicz; TISSUE=Leaf;  
 RX MEDLINE=92056780; PubMed=234100;

[3] — SEQUENCE OF 24-270.  
 RC MEDLINE=92056789; PubMed=234199;  
 RA Collins E.J.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,  
 RT "Isolation and DNA sequence of gene encoding alpha-trichosanthin, a  
 type I ribosome-inactivating protein.";  
 RL J. Biol. Chem. 265:8670-8674 (1990).

[4] — SEQUENCE OF 24-270.  
 RC TISSUE=Tuberous root;  
 RA Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,  
 RA Tian G.Y., Ni C.Z.;  
 RT "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and  
 application.";  
 RL Pure Appl. Chem. 58:789-798 (1986).

[5] — X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE=941344957; PubMed=8066085;  
 RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;  
 RT "Structure of trichosanthin at 1.88 Å resolution.";  
 RL Proteins 19:4-13 (1994).

[6] — X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE=95344383; PubMed=7619070;  
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;  
 RT "Studies on crystal structures, active-centre geometry and  
 depurinating mechanism of two ribosome-inactivating proteins.";  
 RL Biochem. J. 308:285-298 (1995).  
 CC -!- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS  
 CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT IS  
 INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.  
 CC -!- CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one  
 specific adenine on the 28S rRNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 TYPE 1 RIP SUBFAMILY.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to license@isb-sib.ch).

DR EMBL; M3485B; AAA34207.1; -;  
 DR PIR; JT0566; RL7ZT.  
 DR PDB; IMRJ; 07-FEB-95.  
 DR PDB; IMRK; 07-FEB-95.  
 DR PDB; ITC5; 10-JUL-95.  
 DR PDB; IJ4G; 28-JAN-03.

DR PDB; 1NLU; 21-JAN-03.  
 DR PDB; 1QD2; 24-APR-00.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGANICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KW Toxin; Signal; 3D-structure.  
 FT SIGNAL; 1 23  
 FT CHAIN; 24 270  
 RIBOSOME-INACTIVATING PROTEIN ALPHA-  
 TRICHOSANTHIN  
 MISSING IN MATURE PROTEIN.  
 BY SIMILARITY.  
 IPLL -> LPLI (IN REF. 4).  
 MISSING (IN REF. 4).  
 I -> L (IN REF. 4).  
 V -> VDAGIPRNVL (IN REF. 4).  
 KI -> GL (IN REF. 4).  
 K -> S (IN REF. 4).  
 WS -> LML (IN REF. 4).  
 Q -> T (IN REF. 4).  
 S -> T (IN REF. 2).  
 MISSING (IN REF. 4).  
 T -> M (IN REF. 2).

FT PROPEP 271 289  
 ACT SITE 183 183  
 CONFLICT 57 60  
 FT PROPEP 271 289  
 ACT SITE 183 183  
 CONFLICT 82 84  
 FT PROPEP 271 289  
 ACT SITE 183 183  
 CONFLICT 87 87  
 FT PROPEP 271 289  
 ACT SITE 183 183  
 CONFLICT 92 92  
 FT PROPEP 271 289  
 ACT SITE 143 143  
 CONFLICT 196 196  
 FT PROPEP 271 289  
 ACT SITE 215 215  
 CONFLICT 231 231  
 FT PROPEP 271 289  
 ACT SITE 234 234  
 CONFLICT 246 266  
 FT PROPEP 271 289  
 ACT SITE 247 247  
 STRAND 25 28  
 FT PROPEP 271 289  
 ACT SITE 231 231  
 CONFLICT 234 234  
 FT PROPEP 271 289  
 ACT SITE 234 234  
 CONFLICT 246 266  
 FT PROPEP 271 289  
 ACT SITE 247 247  
 STRAND 57 60  
 FT PROPEP 271 289  
 ACT SITE 66 66  
 HELIX 70 70  
 FT PROPEP 271 289  
 ACT SITE 78 78  
 TURN 47 47  
 FT PROPEP 271 289  
 ACT SITE 82 82  
 STRAND 50 54  
 FT PROPEP 271 289  
 ACT SITE 89 89  
 TURN 55 56  
 FT PROPEP 271 289  
 ACT SITE 93 93  
 STRAND 99 99  
 FT PROPEP 271 289  
 ACT SITE 100 100  
 TURN 101 101  
 FT PROPEP 271 289  
 ACT SITE 105 105  
 STRAND 109 114  
 FT PROPEP 271 289  
 ACT SITE 115 115  
 TURN 117 117  
 FT PROPEP 271 289  
 ACT SITE 120 120  
 TURN 121 121  
 FT PROPEP 271 289  
 ACT SITE 124 124  
 STRAND 127 127  
 FT PROPEP 271 289  
 ACT SITE 134 134  
 HELIX 141 142  
 FT PROPEP 271 289  
 ACT SITE 145 147  
 HELIX 150 150  
 FT PROPEP 271 289  
 ACT SITE 152 152  
 STRAND 163 163  
 FT PROPEP 271 289  
 ACT SITE 164 164  
 TURN 165 165  
 FT PROPEP 271 289  
 ACT SITE 167 167  
 HELIX 180 180  
 FT PROPEP 271 289  
 ACT SITE 181 181  
 HELIX 182 186  
 FT PROPEP 271 289  
 ACT SITE 187 187  
 STRAND 188 195  
 FT PROPEP 271 289  
 ACT SITE 196 196  
 TURN 202 202  
 FT PROPEP 271 289  
 ACT SITE 205 226  
 HELIX 227 230  
 FT PROPEP 271 289  
 ACT SITE 231 239  
 STRAND 241 242  
 FT PROPEP 271 289  
 ACT SITE 245 250  
 TURN 251 252  
 FT PROPEP 271 289  
 ACT SITE 254 258  
 HELIX 259 260  
 FT PROPEP 271 289  
 ACT SITE 263 263  
 STRAND 263 263  
 FT PROPEP 271 289  
 ACT SITE 266 268  
 SEQUENCE 289 AA; 31676 MW; 5CE09BB630575BB9 CRC64;  
 Query Match 34.5%;  
 Best Local Similarity 38.9%;  
 Matches 72; Conservative 42; Mismatches 49; Indels .22; Gaps 5;

QY 10 INFITAGATVQSYTNFIRAVRGRLTVLN-----RVGLDINOREFILVELSNIAEL 59  
 DB 25 VSPLSGATSSSSTVGFISNL-KALNNERKLYDPLRSIPLSPGSQPYALLHNTYADE 81  
 QY 60 SVTIALDTNVAYVGYRAGNSAYFFHPDNQEDA-EAITHLFTIVQNRTTFAFGGNYDRLE 118  
 DB 82 TISVIAIDTINVAYMGYRAGDTSYF--NEASATAAKVFDAMRKVTLPLPSGNYERLQ 138  
 QY 119 QLAGNLRENIELENGPLPESALISALYYSTGGTQLPTLARSFLICQIMISEARFOYIE 178  
 DB 139 TAAGKIRENTIPGLPALSATTLFYVAN---SAASALMVLIOSTSEARYKFTEQQ 193  
 QY 179 MRTTRI 183  
 DB 194 IGKRV 198

**RESULT 4**  
**ABRC\_ABPR** STANDARD; PRT; 562 AA.  
**ID P23590;**  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Abrin-c precursor [Contains: Abrin-c A chain (rRNA N-glycosidase)  
 DE (EC 3.2.22.; Abrin-c B chain).]  
 OS Abrus precatorius (Indian licorice) (Crab's eye).  
 OC Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophytina; Magnoliophyta; eudicots; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreidae; Abrus.  
 OX NCBI\_TaxID=3116;  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=leaf;  
 RA Wood K.A., Lord J.M., Wawrzynczak E.J., Piatak M.;  
 RT "PreproAbrin: genomic cloning, characterisation and the expression of  
 the A-chain in Escherichia coli.";  
 RL Eur. J. Biochem. 198:723-732 (1991).  
 CC -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN  
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 6S RIBOSOMAL  
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S rRNA. THE  
 CC B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE  
 CC BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
 CC -!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN  
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-  
 CC -!- INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.

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CC EMBL: X55667; CAA31202.1; -.  
 DR PIR: S16022; S16022.  
 DR HSSP; P1140; IABR.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; Ricin\_B\_lectin; 6.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR SMART; SM0458; RICIN; 2.  
 DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;

KW Glycoprotein; Lectin; Signal; Pyrrolidone carboxylic acid.  
 FW SIGNAL 1 34  
 FT CHAIN 35 285  
 FT PEPTIDE 286 295  
 FT CHAIN 296 562  
 FT DOMAIN 307 434  
 FT DOMAIN 437 561  
 FT REPEAT 317 359  
 FT REPEAT 360 400  
 FT REPEAT 403 435  
 FT REPEAT 448 483  
 FT REPEAT 487 526  
 FT REPEAT 529 562  
 FT ACT SITE 198 198  
 FT DISULFID 281 303  
 FT DISULFID 320 339  
 FT DISULFID 363 380  
 FT DISULFID 451 464  
 FT DISULFID 490 507  
 FT MOD\_RES 35 35  
 FT CARBOHYD 234 234  
 FT CARBOHYD 395 395  
 FT CARBOHYD 435 435  
 SQ SEQUENCE 562 AA; 62817 MW; 1F0DAECD7/BA6278 CRG64;  
 Query Match Score 327.5; DB 1; Length 562;  
 Best Local Similarity 43.9%; Pred. No. 5.3e-23;  
 Matches 82; Conservative 22; Mismatches 68; Indels 15; Gaps 4;

QY 6 QPYLINFATAGATVQSYTNFIRAVRGLT-----VLPNRVGLPIMQRFLIVELSMA 57  
 RN 35 QDQYIKFETEGATQSOKQFTEALRQITGLHDIPVLPDPPTVBRNRYTVELSNE 94  
 DB 58 ELSVTLALDVTVAYVGVRAGNSAYFFPDNOEDAEATHLFTDVQRNTFAGGNYDRL 117  
 DB 95 RESLEVGIDVTVAYWVAXRAGSOSYFL--RDAPASASTYLPGTQ-RYSLRFDGSYCDL 150  
 QY 118 EOLAGLNRLTENIELNGNPLEEAISALYYSTGGTQPLTFLARSFLICQIMISEARFOYEG 177  
 DB 151 ERYAHQTREISLGLQALTHAIS---FLRSGASNDEEKARTLVIVIONASEARYRTSN 207  
 QY 178 EMETRIR 184  
 DB 208 RGVSVIR 214

RESULT 5  
 RES\_PIRKI STANDARD; PRT; 289 AA.  
 ID P24478;  
 AC P24478  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein karasurin precursor (rRNA  
 DE N-glycosidase) (EC 3.2.2.22).  
 OS Trichoanthus kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthaceae; Trichosanthus.  
 OX NCBI\_TaxID=3677;  
 RN 1] SEQUENCE FROM N.A.  
 RX TISSUE=Root tube;  
 RX MEDLINE=97356562; PubMed=9212998;  
 RA Mizukami H.; Iida K.; Kondo T.; Ogihara Y.;  
 RT "Cloning and bacterial expression of a gene encoding ribosome-  
 inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes  
 kirilowii var. japonica.";  
 RT Biol. Pharm. Bull. 20:711-713 (1997).  
 RN 2] SEQUENCE OF 24-270.  
 RX MEDLINE=92005921; PubMed=1914000;

RA	Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.; RT "The complete amino acid sequence of an abortifacient protein, RT karasurin.", RT Chem. Pharm. Bull. 39:1244-1249(1991).	MEDLINE=913132798; PubMed=8421313;
RL	-	Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.; RT "Primary structure of three distinct isoabrinins determined by cdNA sequencing, Conservation and significance.", J. Mol. Biol. 229:263-267(1993).
CC	-	[2]
CC	-	SEQUENCE OF 260-527.
CC	-	SEQUENCE OF 260-527.
CC	-	TISSUE=Seed;
RC	-	RC TISSUE=Seed;
RA	"The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic proteins from the seeds of Abrus precatorius.", Kimura M., Sumizawa T., Funatsu G.; RT Biosci. Biotechnol. Biochem. 57:166-169(1993).	
RT	-	FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4, 324 OF 28 S RNA.
RL	-	ABRIN-A IS MORE TOXIC THAN RICIN.
RN	-	FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
RA	-	CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S RNA.
RT	-	SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
RL	-	DOMAIN: THE CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC	-	SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC	-	SIMILARITY: Contains 2 ricin B-type lectin domains.
CC	-	CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S RNA.
CC	-	SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC	-	DOMAIN: THE CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC	-	SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC	-	SIMILARITY: Contains 2 ricin B-type lectin domains.
CC	-	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
CC	-	CC SIGNAL 1 21 POTENTIAL.
CC	FT CHAIN 22 270 KARASURIN-C.	
CC	FT CHAIN 24 270 KARASURIN-A.	
CC	FT PROPEP 271 289 REMOVED IN MATURE FORM.	
CC	FT ACT SITE 183 183 BY SIMILARITY.	
CC	FT SEQUENCE 289 AA; 31704 MW; 883D3E3242887B26 CRC64;	
CC	Query Match Best Local Similarity 33.4%; Score 326; DB 1; Length 289; Matches 72; Conservative 44; Mismatches 50; Indels 16; Gaps 5;	
CC	10 INFTTAGATVQSYTNFIRAVR-----GRLTVLP-NEVGLIPINQRFLIVEJSNHAEIHSV 62 DR PIR: S32430; S32430.	
CC	25 VSPRLSGATSSYYGVFISNLKALPYERKLVNIPLRLSTLPSQRVALIHLTNAYETIS 84 DR HSSP; P11140; IABR.	
DB	63 LALDVINAYVVGVRAGNSAYFFHPDNQEDA-BAITHLFTDVNRYTFAGGGNYDRLEQLA 121 DR InterPro; IPR001574; RIP.	
DB	85 VAIDVNTVNYVGYRAGDTSYF--NEASATVAAKTYFKDAKRVTLIPSSGYNERIQIAA 141 DR InterPro; IPR001572; Ricin_B_LECTIN.	
DB	122 GNLRNTELGNGPLEEAATSLAYYLYSTGGCTQPLTARSFIUQOMISPAARFOYIEGEMRT 181 DR PROSITE; PS00231; RICIN_B_LECTIN.	
DB	142 GKTRNENPLGLPALSATLTFIYNAN---SAASALMVLQTSAAKYKPFQDQIGK 196 DR PROSITE; PS00235; SHIGA_RICIN.	
DB	182 RI 183 FT PEPTIDE 251 260 LINKER PEPTIDE.	
DB	197 RV 198 FT CHAIN 261 527 ABRI-N B-CHAIN.	
DB	FT DOMAIN 272 399 RICIN B-TYPE LECTIN 1.	
DB	FT DOMAIN 402 526 RICIN B-TYPE LECTIN 2.	
DB	FT REPEAT 282 324 1-ALPHA.	
DB	FT REPEAT 325 365 1-BETA.	
DB	FT REPEAT 368 400 1-GAMMA.	
DB	FT REPEAT 413 448 2-ALPHA.	
DB	FT REPEAT 452 491 2-BETA.	
AC	Q06077; P81374; STANDARD; DT 15-DEC-1998 (Rel. 37, Created)	FT REPEAT 494 527 2-GAMMA.
DT	15-DEC-1998 (Rel. 37, Last sequence update)	FT ACT SITE 163 163 INTERCHAIN (BY SIMILARITY).
DT	28-FEB-2003 (Rel. 41, Last annotation update)	FT DISULFID 246 268 BY SIMILARITY.
DE	Abra-in-b Precursor [Contains: Abra-in-b A chain (rRNA N-glycosidase)]	FT DISULFID 285 304 BY SIMILARITY.
DE	(EC 3.2.2.22); Abra-in-b B chain].	FT DISULFID 328 345 BY SIMILARITY.
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids 1; Fabales; Fabaceae; Papilionoideae; Abraeae; Abrus.	FT DISULFID 416 429 BY SIMILARITY.
OC	[1] NCBI_TAXID=31816;	FT MOD_RES 455 472 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
OC	SEQUENCE FROM N.A.	FT CARBOYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
OX		FT CARBOYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
RN		FT CARBOYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
RP		N > D (IN REF. 2).



PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RIBOSOMAL B CHAIN IN A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE ENDOCYTOSIS.

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 28S rRNA.

CC -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.

CC -!- SIMILARITY: IN THE N-TERMINAL SECTION BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.

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CC EMBL; U41299; AAB39475.1; - . DR PIR; S37382; S37382; InterPro; IPR000772; Ricin\_B\_lectin. DR IPR0001574; Ricin\_B\_lectin. 6. PFam; PF00652; Ricin\_B\_lectin. 6. PFam; PF00161; RIP; 1. DR PRINTS; PRO00396; SHIGARICIN. SMART; SMM00458; RICIN; 2. PROSITE; PS00275; SHIGA\_RICIN; 1. DR PS00231; RICIN\_B\_LECTIN; 2. DR plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; KW Glycoprotein; Lectin; Signal.

FT SIGNAL 1 25 FT CHAIN 26 297 FT CHAIN 298 563 FT DOMAIN 305 431 FT DOMAIN 434 559 FT REPEAT 316 356 FT REPEAT 357 397 FT REPEAT 400 432 FT REPEAT 445 482 FT REPEAT 486 524 FT REPEAT 527 554 FT ACT\_SITE 188 188 FT DISULFID 274 302 FT DISULFID 319 338 FT DISULFID 360 377 FT DISULFID 448 463 FT DISULFID 489 505 FT CARBOHYD 221 221 FT CARBOHYD 368 368 FT CARBOHYD 376 376 FT CARBOHYD 483 483 FT CARBOHYD 537 537 FT CONFLICT 39 39 K > V (IN REF. 2) SQ SEQUENCE 563 AA; MW: 62300 MW; F25003E24621BF14 CRC64;

Query Match Score 307.5%; DB 1; Length 563; Best Local Similarity 38.4%; Pred. No. 3.9e-21; Matches 73; Conservative 36; Mismatches 56; Indels 25; Gaps 5;

Qy 7 YPLINFETGAVYQSINTNIFRAV-----GRITFLDPVRGVDFINQFLVELSNH 56

Db 28 YPSVSFNIDGAKSATVDFLSURKTVATGTYEVNGIPIVLFRESEYQVKSFVLYPLTNY 87

Qy 57 AEISVTLADIVNAYVGYRAGNSAYSFHPDNQDEAFAI-THLFTDVQNYTFAGGNY 114

Db 98 NGNTVILANDVNLVYVAFSGNANSIFF---KDATEVQGSNLFGTKNI-TLSPTGNY 141

Qy 115 DRLQLAGNLRENTIELNGPPEEAISALYYYSTGGCQLPTLARSFLICQIMISEARFOY 174

Db 142 DNLETANTRRESIELGPSPLDGAITSLYHDD-----SVARSLLVVIQMVSEARFRY 194

Qy 175 LEGEMTRIR 184

Db 195 TEQEVEVSLQ 204

RESULT 9

RIP1\_BRYDI ID RIP1\_BRYDI STANDARD; PRT; 290 AA.

AC P33185; OSB819; DT 01-OCT-1993 (Rel. 27, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ribosome-inactivating protein bryodin 1 precursor (rRNA N-glycosidase) (EC 3.2.2.22) (BD1).

DE Bryonia dioica (Red bryony).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyt; Magnoliophyt; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitaceae; Bryonia.

NCBI TaxID=3652; [1] \_

RN SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).

RP TISSUE=Leaf; MEDLINE=97228081; PubMed=9115985;

PX Gawlik S.L.; Neubauer M.; Klei H.E.; Chang C.Y.Y.; Einspahr H.M., Siegall C.B.;

RA "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant Bryonia dioica"; RT Biochemistry 36:3095-3103 (1997). [2]

RN SEQUENCE FROM N.A.

RP Cloning and expression of a gene encoding bryodin 1 from Bryonia dioica."; RT Patent number US5541110, 30-JUL-1996.

RA Siegall C.B.;

RA "Cloning and expression of a gene encoding bryodin 1 from Bryonia dioica."; RT Sequence of [3]

RN Sequence of 24-66.

RP TISSUE=Seed; MEDLINE=89326691; PubMed=2753596;

RA Montecuccchi P.C.; Lazzarini A.M.; Barbieri L.; Stirpe F.; Soria M., Lappi D.; RT "N-terminal sequence of some ribosome-inactivating proteins."; RL Int. J. Pept. Protein Res. 33:263-267 (1989). [4]

RN Sequence of 24-43.

RP TISSUE=Root; MEDLINE=95151812; PubMed=7849072;

RA Siegall C.B.; Gawlak S.L.; Chace D.; Wolff E.A., Mixan B., Margardt H.; RT "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunoconjugates."; RL Bioconjug. Chem. 5:433-439 (1994). CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS.

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -!- PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO PRODUCE A SHORTER PROTEIN.

CC -!- BIOTECHNOLOGY: Especially useful as immunotoxin for pharmaceutical applications as it has low toxicity in rats and mice but is potent once inside target cells.

CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 1 RIP SUBFAMILY.

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CC	or send an email to license@isb-sib.ch.
CC	EMPB; T24020; -; NOT_ANNOTATED_CDS.
DR	PFR; S16491; S16491.
DR	PDB; 1BYV; 04-MAR-98.
DR	InterPro; IPR001574; RIP.
DR	PFam; PF00161; RIP; 1.
DR	PROSITE; PS00275; SHIGA_RICIN.
DR	Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
KW	3D-structure; Multigene family; Glycoprotein; Signal.
FT	SIGNAL 1 23
FT	CHAIN 24 270 RIBOSOME INACTIVATING PROTEIN BRYODIN I.
FT	PROPEP 271 290 MISSING IN MATURE PROTEIN.
FT	ACT SITE 183 BY SIMILARITY.
FT	ACT-SITE 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MUTAGEN 212 212 E>K: REDUCES ACTIVITY 10-FOLD.
FT	CONFLICT 212 212 RSSS -> LRRH1 (IN REF. 3).
FT	STRAND 25 28 (EC 3.2.2.2); Abrin-a B chain.
FT	TURN 30 31 Abrus Precatorius (Indian licorice) (Crab's eye).
FT	HELIX 34 46 Eukaryota; Viridiplantae; Streptopteryta; Embryophyta; Tracheophyta;
FT	TURN 47 47 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
FT	STRAND 50 54 eurosids I; Fabales; Fabaceae; Papilioideae; Aburiae; Abrus.
FT	TURN 55 56 NCBI_TaxID=3816;
FT	STRAND 57 60 [1] RN SEQUENCE FROM N.A.
FT	HELIX 66 69 RX MEDLINE=8421313;
FT	STRAND 70 76 TISSUE_Seed; PMID=9313279;
FT	TURN 78 79 DT 01-JUL-1989 (Rel. 11, Created)
FT	STRAND 82 88 DT 01-JUN-1994 (Rel. 29, Last sequence update)
FT	TURN 89 92 DT 28-FEB-2003 (Rel. 41, Last annotation update)
FT	STRAND 93 99 DE Abrin-a Precursor (Contains: Abrin-a A chain (rRNA N-glycosidase))
FT	TURN 100 101 DE (EC 3.2.2.2); Abrin-a B chain.
FT	STRAND 102 105 DE OS Abrus Precatorius (Indian licorice) (Crab's eye).
FT	HELIX 109 114 DE OC Eukaryota; Viridiplantae; Streptopteryta; Embryophyta; Tracheophyta;
FT	TURN 115 117 DE OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
FT	STRAND 120 121 DE OC eurosids I; Fabales; Fabaceae; Papilioideae; Aburiae; Abrus.
FT	TURN 124 127 DE OX NCBI_TaxID=3816;
FT	STRAND 134 141 RN [2] SEQUENCE OF 1-251.
FT	TURN 142 142 RN RX TISSUE_Leaf; PMID=91201329;
FT	STRAND 145 147 RN RX "Direct molecular cloning and expression of two distinct abrin
FT	HELIX 150 150 RN RX A-chains.";
FT	STRAND 152 163 RN RX Evensen G.; Mathiesen A.; Sundan A.;
FT	TURN 164 165 RN RX "The complete primary structure of abrin-a B chain.";
FT	HELIX 167 186 RN RX Tahlirov T.H.; Lu T.-H.; Liaw Y.-C.; Chen Y.-L.; Lin J.-Y.;
FT	STRAND 187 187 RN RX "The complete primary structure of abrin-a B chain.";
FT	HELIX 188 196 RN RX FEBS Lett. 309:115-118 (1992).
FT	STRAND 202 202 RN RX [4] SEQUENCE OF 262-528.
FT	HELIX 206 213 RN RX MEDLINE=92311656; PubMed=1505674;
FT	TURN 214 214 RN RX Chen Y.-L.; Chou L.-P.; Tsugita A.; Lin J.-Y.;
FT	HELIX 215 225 RN RX "The complete primary structure of abrin-a B chain.";
FT	TURN 226 230 RN RX RL J. Mol. Biol. 250:354-367 (1995).
FT	STRAND 231 239 RN CC -I- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
FT	TURN 241 244 RN CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
FT	STRAND 245 250 RN CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4.324 OF 28 S RNA.
FT	TURN 251 252 RN CC ABRIN-A IS MORE TOXIC THAN RICIN.
FT	HELIX 254 257 RN CC -I- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
FT	TURN 258 259 RN CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
FT	STRAND 260 260 RN CC PRECEDES ENDOCYTOSIS.
FT	STRAND 263 263 RN CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
FT	HELIX 266 268 RN CC specific adenosine on the 28S rRNA.
FT	SEQUENCE 290 AA; 31728 MW; E966CD9C031A42DB CRG64; RN CC -I- SUBUNITS: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
Query	10 INFETTAGTVQSYNTNFTRAVRGRLLTVDLNRYGLPI-----NQRFLVLENHAEISVT 62 CC -I- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
Db	25 VSPRLSGATTTSVGETKRNREALPYERKVYNPLRSSGRTLHTVNADETIS 84, CC -I- CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
Qy	63 LALDVTNAYVGYRAGNSAYFFHPDNQEDA-EATHLFTDVQNTYFAFGGNYDRLEQLA 121 CC -I- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-

CC INACTIVATING PROBIN FAMILY. TYPE 2 RIP SUBFAMILY.  
 CC !- SIMILARITY: Contains 2 ricin B-type lectin domains.

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 CC or send an email to license@isb-sib.ch).

CC DR M98344; AAA32624\_1; ALT INIT.  
 DR EMBL; X54872; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; S32429; TZLSA.  
 DR PDB; 1ABR; 07-FEB-95.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RICP.  
 DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam; PF00161; RICP; 1\_lectin; 6.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR SMART; SMD0458; SHIGARICIN.  
 DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 DR PROSITE; PS500275; SHIGA\_RICIN; 1.  
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 KW Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.  
 FT CHAIN 1 251 ABIN-A A CHAIN.  
 FT PEPTIDE 252 261 LINKER PEPTIDE.  
 FT DOMAIN 262 528 ABIN-A B CHAIN.  
 FT DOMAIN 273 400 RICIN B TYPE LECTIN 1.  
 FT REPEAT 403 527 RICIN B-TYPE LECTIN 2.  
 FT REPEAT 283 325 1-ALPHA.  
 FT REPEAT 326 366 1-BETA.  
 FT REPEAT 369 401 1-GAMMA.  
 FT REPEAT 414 449 2-ALPHA.  
 FT REPEAT 453 492 2-BETA.  
 FT REPEAT 495 528 2-GAMMA.  
 FT ACT SITE 164 264 BY SIMILARITY.  
 FT DISULFID 247 269 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 286 305 BY SIMILARITY.  
 FT DISULFID 329 346 BY SIMILARITY.  
 FT DISULFID 417 430 BY SIMILARITY.  
 FT DISULFID 456 473 BY SIMILARITY.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT CARBOHYD 361 361 N-LINKED (GLCNAC. ).  
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. ).  
 FT CONFLICT 202 MISSING (IN REF. 2).  
 FT CONFLICT 298 N -> Y (IN REF. 4).  
 FT CONFLICT 427 427 M -> L (IN REF. 4).  
 FT CONFLICT 467 467 T -> P (IN REF. 4).  
 FT CONFLICT 483 483 V -> L (IN REF. 4).  
 FT STRAND 5 8  
 FT TURN 10 11  
 FT HELIX 14 28  
 FT STRAND 32 33  
 FT TURN 34 35  
 FT STRAND 36 38  
 FT TURN 42 43  
 FT HELIX 47 49  
 FT STRAND 51 57  
 FT STRAND 63 69  
 FT TURN 70 72  
 FT STRAND 75 79  
 FT TURN 83 86  
 FT TURN 88 93  
 FT TURN 92 93  
 FT HELIX 94 97  
 FT TURN 100 101  
 FT STRAND 103 106  
 FT TURN 113 114  
 FT HELIX 115 119  
 FT TURN 124 126  
 FT STRAND 129 129  
 FT HELIX 131 142

FT TURN 143 144  
 FT HELIX 148 167  
 FT STRAND 168 168  
 FT HELIX 169 180  
 FT TURN 181 182  
 FT STRAND 185 185  
 FT HELIX 189 196  
 FT TURN 197 197  
 FT HELIX 198 207  
 FT STRAND 212 220  
 FT TURN 222 223  
 FT TURN 226 231  
 FT TURN 232 233  
 FT HELIX 235 239  
 FT STRAND 240 240  
 FT STRAND 243 243  
 FT TURN 248 248  
 FT STRAND 268 268  
 FT STRAND 276 277  
 FT STRAND 279 280  
 FT HELIX 282 284  
 FT STRAND 286 289  
 FT HELIX 290 292  
 FT TURN 296 297  
 FT STRAND 299 303  
 FT HELIX 311 313  
 FT STRAND 315 317  
 FT TURN 319 320  
 FT STRAND 322 325  
 FT TURN 326 327  
 FT STRAND 328 332  
 FT TURN 337 338  
 FT STRAND 340 344  
 FT TURN 346 348  
 FT HELIX 351 353  
 FT STRAND 355 355  
 FT STRAND 357 358  
 FT TURN 360 361  
 FT STRAND 364 366  
 FT TURN 367 370  
 FT STRAND 371 374  
 FT TURN 380 381  
 FT STRAND 383 383  
 FT STRAND 385 387  
 FT HELIX 393 395  
 FT STRAND 398 399  
 FT STRAND 406 408  
 FT TURN 410 411  
 FT HELIX 413 415  
 FT STRAND 417 421  
 FT TURN 422 423  
 FT STRAND 424 428  
 FT TURN 432 433  
 FT HELIX 435 437  
 FT STRAND 439 441  
 FT TURN 443 444  
 FT STRAND 447 449  
 FT TURN 450 451  
 FT STRAND 452 459  
 FT TURN 464 465  
 FT STRAND 467 472  
 FT TURN 474 475  
 FT HELIX 478 480  
 FT STRAND 483 484  
 FT TURN 486 487  
 FT STRAND 490 492  
 FT TURN 493 496  
 FT STRAND 497 501

Query Match 31.1%; Score 303.5; DB 1; Length 528;  
 Best Local Similarity 41.1%; Pred No. 8.6e-21;  
 Matches 76; Conservative 26; Mismatches 64; Indels 19; Gaps 5;

10 INFTTAGATVQSYTINFIRAVRGRU-----TVLPNRVGLPINQRFTLVELSNHAEILSV 61  
 5 IKFSEGATSSQSYKTFIEALRGRGLIHDIPVLPDTTLQERNRYTIVELNSNHTESI 64

62 TLAIDVTNAYVGYRAGNSAYFFPFDNQDAEAITHLFTDYNRTPAFCGNYDRLEQ 119  
 65 EVDGLDVMTAVYAVRAGTOSYFLERDAPSSAASD----YIFTGT-DQHSIPFPGYGDLLR 118

120 LAGNURLENELGNGPLEEAIASALYYSTGGTQLPTLARSFLICOMISARFOYIEGM 179  
 119 WAHQSRQQIPFLGQLATHGS---FERSGGNDNEEKARTLIVITQMAEARFRYISNRV 175

180 RTRIR 184  
 Db 176 RVSTIQ 180

RESULT 11  
 RIPI\_LUFCY STANDARD; PRT; 250 AA.  
 AC P22851;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein luffin-B (tRNA N-glycosidase)  
 DE (EC 3.2.2.22).  
 OS Luffa cylindrica (Smooth loofah) (Sponge gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;  
 OC euroids I; Cucurbitales; Cucurbitaceae; Luffa.  
 RN [1] \_TaxID=3670;  
 RP SEQUENCE.  
 RC TISSUE-Seed;  
 RX MEDLINE-91248498; PubMed=1368666;  
 RA Islam M.R., Hirayama H., Funatsu G.;  
 RT "Complete amino acid sequence of luffin-b, a ribosome-inactivating  
 protein from sponge gourd (Luffa cylindrica) seeds.";  
 RL Agric. Biol. Chem. 55:229-238 (1991).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 specific adenine on the 28S rRNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.

DR PIR; JN0108; JN0108.  
 DR HSSP; P16094; LAHC.  
 DR InterPro; IPR001574; RIP.  
 DR PFAM; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KW Toxin; Signal. 1 21  
 FT SIGNAL 1 21  
 FT CHAIN 22 286  
 DR ACT SITE 185 185  
 DR CARBOHYD 103 103  
 DR CARBOHYD 110 110  
 DR CARBOHYD 252 252  
 SQ SEQUENCE 286 AA; 31771 MW; 4EFD4966Bc04DA11 CRC64;

Query Match 28.9% Score 281.5; DB 1; Length 286;  
 Best Local Similarity 32.4%; Pred. No. 4\_6e-19;  
 Matches 60; Conservative 46; Mismatches 64; Indels 15; Gaps 3;

QY 10 INFTTAGATVQSYTINFIRAVRGRU-----TVLPNRVGLPINQRFTLVELSNHAEILSVT 62  
 3 VFSLSGADSKSYSKFITALKRALPSKERVNSNPLIPSASSGA--SRYILMOLSNYDAK 59  
 60 SVTIALDNTNAYVGYRAGNSAYFFPFDNQDAEAITHLFTDYNRTPAFCGNYDRLEQ 119  
 60 AITMAIDVTNAYVGYRAGNSAYFFPFDNQDAEAITHLFTDYNRTPAFCGNYDRLEQ 116  
 120 LAGNURLENELGNGPLEEAIASALYYSTGGTQLPTLARSFLICOMISARFOYIEGM 179  
 117 AGKIREKIPGLPRAEDSALTSHYD---TAAAFAVLVIQTAEARSKYIEGQI 171  
 180 RTRIR 186  
 172 IERIPKN 178

Db 200 ISVSK 204

RESULT 13

RIPALUCY		STANDARD;	PRT;	277 AA.	
AC	000465;				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last annotation update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Ribosome-inactivating protein luffin-alpha precursor (tRNA N-glycosidase) (EC 3.2.2.2).				
DE	Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Momordicae; OC				
OC	NCBI_TaxID=3673;				
OX	[1]				
RN	SEQUENCE FROM N.A.				
RC	TISSUE-Seed;				
RX	PubMed=1600156;				
RA	Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.; "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating protein from Luffa cylindrica.";				
RT	Plant Mol. Biol. 18:1199-1202 (1992).				
RL	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 28S rRNA.				
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.				
CC	TYPE 1 RIP SUBFAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to licensee@isb-sib.ch).				
CC	EMBL: X62371; CA44229.1; -.				
DR	PIR: S22494; S22494.				
DR	HSSP: P16094; 1AHC.				
DR	InterPro: IPR001574; RIP.				
DR	PFAM: PF00161; RIP; 1.				
DR	PROSITE: PS00275; SHIGRICIN.				
KW	Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase; toxin; Signal.				
FT	SIGNAL 1 19				
FT	CHAIN 20 277				
FT	ACT SITE 179 179				
SQ	SEQUENCE 277 AA; 30212 MW; EA17FC27998025AC CRC64;				
Query Match	28.2%; Score 274.5; DB 1; Length 277;				
Best Local Similarity	33.3%; Pred. No. 2e-18;				
Matches	63; Conservative 42; Mismatches 61; Indels 23; Gaps 5;				
QY	1.0 INFITAGATVQSYNTNFTRAVGRITVLPNRVGLPIN-----QRFILVELSNHAE 58				
Db	22 VRFSLSGSSTSYSKFIGLR--KALPEN-GTVYNINITLSSASGARYNTMLSNYDG 77				
QY	59 LSFTSLAIDTTNAYVGYRANSAYFPDMDQEDAEITHLFDQVNRTFAFGNYDLE 118				
Db	78 KATIVAVDVNVYIMGYLVNSTSYFF--NESDAKLAQSOVFGKSTIVLPGSGNEYKLQ 134				
QY	119 QLAGNLRENTLGNGPLERAISALYYSTGQLPQLTARSFLICQIMSEAAFKQYIEGE 178				
Db	135 TAAKIREKPLGPALSAITIPLHYD-----TAAKAFIVIQTAAESPKYIEGQ 189				
QY	179 MRTIRYNR 187				
Db	190 IIERISRNQ 198				
RESULT 14					
RIP1_MONCH					
ID	RIP1_MONCH STANDARD;				
	PRT;	286 AA.			



Db 141 KIRENIDGLPALSSAITLFFYNA-----QSAPSALLVLIQTTAEAAARFKYTERHVAKY 195  
Qy 183 TRYN 186  
: :  
Db 196 VATN 199

Search completed: February 10, 2004, 16:23:26  
Job time : 6.33803 secs

GenCore version 5.1.6  
(c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:00 ; Search time 25.3521 Seconds  
(without alignments)  
1933.961 Million cell updates/sec

Title: US-10-083-336A-11

Perfect score: 975

Sequence: 1 MLEPKQYDILNFTTAGATVQ.....RFQYIEGEMRTRIYNRRSA 190

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched:

830525 seeds, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp Rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Q38761	abrus preca
Q04071	sambucus ni
Q00980	luffa cylindrica
Q9MGEB9	abrus preca
Q96236	abrus preca
Q96237	abrus preca
Q04072	sambucus ni
Q96235	abrus preca
Q9F5H2	momordica c
Q41358	sambucus ni
Q8We7	iris hollian
Q9fAv7	momordica c
Q2415	sambucus ni
Q9F5F5	polygonatum
Q41257	momordica c
Q8W243	viscum albu
Q8LKG6	viscum albu
Q8We8	iris hollian
Q8lkq4	viscum albu
Q95452	jatropha cu
P93543	sambucus ni
Q8rxh6	viscum albu
Q8rxh7	viscum albu
Q9s8e4	gelonium mu
Q8yyu0	jatropha cu
Q8YF69	Gynostemma
Q8nY4	Gynostemma
Q9mt53	Polygonatum

#### ALIGNMENTS

#### RESULT 1

Q41174	ID	Q41174; PRELIMINARY;	PRT;	541 AA.
AC	DT	01-NOV-1996 (TREMBLrel. 01, Created)		
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
	DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DB	DE	Pro ricin A chain (EC 3.2.2.22) (rRNA N-glycosidase)		
OS	DE	(Fragment).		
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; euroids I; Malpighiales; Euphorbiaceae; Ricinus.			
OX	NCBI_TaxID:3988;			
RN	[1]	SEQUENCE FROM N.A. MEDLINE=92338377; PubMed=1633311; RBL		
RR	Roberts L.M., Tregear J.W., Lord J.M.;			
RT	"Molecular cloning of ricin."			
RL	Targeted Diagn. Ther. 7:81-97 (1992).			
CC	- - CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENINE ON THE 28S rRNA.			
CC	- - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.			
DR	EMBL: S40366; AAB22582.1; -			
DR	SMART: SM00458; Ricin_B_lectin.			
DR	InterPro: IPR001574; RIP.			
DR	InterPro: IPR001400; Somatotropin.			
DR	Pfam: PF00652; Ricin_B_lectin. 6.			
DR	Pfam: PF00161; RIP. 1.			
DR	PRINTS; PRO396; SHIGARICIN.			
DR	SMART: SM00458; Ricin, 2.			
DR	PROSITE: PS50231; RICIN_B_LECTIN; 2.			
DR	PROSITE: PS00275; SHIGA_RICIN; 1.			
DR	Hydrolease; Toxin.			
FT	NON-TER: 1			
SQ	SEQUENCE 541 AA.; 1 60281 MW; 2B7B2CDF1F2E9D9 CRC64;			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	955	97.9	541	0 Q41174
2	372.5	38.4	580	0 Q44bw3
3	370.5	38.2	580	10 Q94bw4
4	368.5	38.0	581	10 Q44bw5
5	368.5	37.8	549	10 Q9Fv22
6	334	34.3	289	10 Q9KE4
7	332	34.1	289	10 Q41216
8	329.5	33.8	563	10 Q04367
9	326	33.4	247	10 Q9fRE3
10	323.5	33.2	564	10 QAVR2
11	318.5	32.7	528	10 Q06076
12	317	32.5	270	10 Q81Pv7
13	310.5	31.8	252	10 Q38760
14	307.5	31.5	563	10 Q958s2
15	307.5	31.5	563	10 Q8QT32
16	305	31.3	270	10 Q41611

Query	Match Score	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps	Y	177 GEMTRI 183
Matches 189; Conservative 0; Mismatches 0;	97.9%; 95.0%;	541;	3e-32;	1				Db	208 YRVRESI 214
Qy	2 IFFPKQPIINFTAGATVQSYTNFIRAVGRIL-----VLPNRVGLPINQRFLV	51							
Db	1 IFFPKQPIINFTAGATVQSYTNFIRAVGRIL-----VLPNRVGLPINQRFLV	60							
									RESULT 3
									Q94BWA
									PRELIMINARY;
									ID Q94BWA ; PRT; 580 AA.
Qy	52 ELSNHAEISVTLAIDTNAYTGYRAGNSAYFFPHQNQDEAITHLFTDVQNRYTFAFG 111							AC Q94BWA ;	
Db	61 ELSNHAEISVTLAIDTNAYTGYRAGNSAYFFPHQNQDEAITHLFTDVQNRYTFAFG 120							DT 01-DEC-2001 (TREMBUREL 19, Created)	
Qy	112 GNYDRLQLAGNLRENTLGNGPLEEAISALYYSTGGTQOPTLARSFIICQIMSEAA 171							DT 01-DEC-2001 (TREMBUREL 19, Last sequence update)	
Db	121 GNYDRLQLAGNLRENTLGNGPLEEAISALYYSTGGTQOPTLARSFIICQIMSEAA 180							DT 01-MAR-2003 (TREMBUREL 23, Last annotation update)	
Qy	172 FQYIEGEMTRI TRYNRSA 190							DE Type 2 ribosome-inactivating protein cinnamomin II precursor (EC 3.2.2.22) (rRNA N-glycosidase).	
Db	181 FQYIEGEMTRI TRYNRSA 199							DB (EC 3.2.2.22) (rRNA N-glycosidase).	
								Cinnamomum camphora (Camphor tree).	
								CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.	
								CC Spermatozoa; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.	
								OC NCBI_TaxID=13429;	
								RN [1] -	
								RP SEQUENCE FROM N.A.	
								RA Yang Q., Gong Z.Z., Liu W.Y.;	
								RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein genes encoding cinnamomin proteins and study of their expression patterns".	
								RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.	
								CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.	
								CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
								DE EMBL; AY039802; RA82459_1; -	
								DR InterPro; IPR00772; Ricin_B_lectin.	
								DR InterPro; IPR001574; RIP.	
								DR Pfam; PF00652; Ricin_B_lectin.	
								DR Pfam; PF00161; RIP; -.	
								DR PRINTS; PR00396; SHIGARICIN.	
								DR SMART; SM00458; RICIN_2.	
								DR PROSITE; PS50231; RICIN_B_LECTIN.	
								FT HYDROLASE; Signal, Toxin.	
								FT SIGNAL. 1 32 POTENTIAL.	
								FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN	
								FT SQ SEQUENCE 580 AA; 64265 MW; 37B4289CC0CBFF CRC64;	
								Query Match 38.2%; Score 372.5; DB 10; Length 580;	
								Best Local Similarity 47.6%; Pred. No. 6.1e-27; Mismatches 56; Indels 15; Gaps 5;	
								RA Yang Q., Gong Z.Z., Liu W.Y.;	
								RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein genes encoding cinnamomin proteins and study of their expression patterns".	
								RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.	
								CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.	
								CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
								DR EMBL; AY039803; RA82460_1; -	
								DR InterPro; IPR00772; Ricin_B_lectin.	
								DR PRINTS; PR001574; RIP.	
								DR Pfam; PF00161; Ricin_B_lectin.	
								DR PRINTS; PR00396; SHIGARICIN.	
								DR SMART; SM00458; RICIN_2.	
								DR PROSITE; PS50231; RICIN_B_LECTIN.	
								FT HYDROLASE; Signal, Toxin.	
								FT SIGNAL. 1 32 POTENTIAL.	
								FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN	
								FT SQ SEQUENCE 580 AA; 64421 MW; 940D1FOF7FB558 CRC64;	
								Query Match 38.4%; Score 374.5; DB 10; Length 580;	
								Best Local Similarity 48.1%; Pred. No. 3.9e-27;	
								Matches 90; Conservative 26; Mismatches 56; Indels 15; Gaps 5;	
								Qy 177 GEMTRI 183	
								Db 208 YRVRESI 214	
								RESULT 4	
								Q94BWS	
								AC Q94BWS ; PRT; 581 AA.	
								DT 01-DEC-2001 (TREMBUREL 19, Created)	
								DT 01-DEC-2001 (TREMBUREL 19, Last sequence update)	
								DT 01-MAR-2003 (TREMBUREL 23, Last annotation update)	
								DE Type 2 ribosome-inactivating protein cinnamomin I precursor (EC 3.2.2.22) (rRNA N-glycosidase).	
								Db 150 LERVAGERETILGMDEPLNEAISALWNLN-QORALARSLIVVQMYAEAVRFIE 207	



Db	82 TISVALIDTVNYVYRAGDTSYFF--NEASATEAKVYFKDSMRKTFIPLPSGNYERLQ	138	Sambucus nigra (European elder).
Qy	119 QLAGNLRLENLGNGLPPEEAISALAYYYSTGGTQLPTLARSLFICIQMISSEAARYIEEG	178	Eukaryota; Viridiplante; Streptophyta; Embryophyta; Tracheophyta;
Db	139 TAAGKIRENTIPGLPALSATITLEYYNAN----SAASALMVLQSTSSEAARYKFIQQ	193	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Qy	179 MRTRI 183		Asteridae; campanulids; Dirosacales; Rosaceae; Sambucus .
Db	194 IGKV 198		NCBI_TaxID=4202;
RESULT 7			[1]
Q41216	PRELIMINARY;	PRT;	289 AA.
AC	Q41216;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		"The major elderberry ( <i>Sambucus nigra</i> ) fruit protein is a lectin
DT	01-OCT-2002 (TREMBLrel. 01, Last sequence update)		" derived from a truncated type 2 ribosome-inactivating protein.";
DB	Trichosanthin (EC 3.2.2.22) (rRNA N-glycosidase).		Plant J. 12:1251-1260 (1997).
GN	TRICHOSANTHIN_TCS.		-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
OS	Trichosanthos kirilowii (Mongolian snake-gourd).		C-C SPECIFIC ADENOSINE ON THE 28S rRNA.
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		CC -!- C-SPECIFIC ADENOSINE ON THE 28S rRNA.
OC	eurosidids II; Cucurbitales; Cucurbitaceae; Trichosanthes .		CC -!- C-SPECIFIC ADENOSINE ON THE 28S rRNA.
OX	NCBI_TaxID=3677;		CC -!- C-SPECIFIC ADENOSINE ON THE 28S rRNA.
RN			CC -!- C-SPECIFIC ADENOSINE ON THE 28S rRNA.
RP	SEQUENCE FROM N.A.		CC -!- C-SPECIFIC ADENOSINE ON THE 28S rRNA.
RX	MEDLINE=94271613; PubMed=8003348;		DR InterPro; IP0001574; RIP.
RA	Zheng H., Wang B., Shaw P., Young H.;		DR Pfam; PF00161; RIP; 1.
RT	"[Cloning and DNA sequencing of the gene encoding trichosanthin]."		DR PRINTS; PR00396; SHIGARICIN.
RL	I Chuan Hsueh Pao 21:42-51(1994).		DR SMART; SM00458; RICIN; 2.
CC	-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE		DR PROSITE; PS50331; RICIN_B_LECTIN; 2.
CC	-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.		DR PROSITE; PS00275; SHIGA_RICIN; 1.
CC	-!- C-SPECIFIC ADENOSINE ON THE 28S rRNA.		KW Hydrolase; Signal; Toxin.
CC	-!- C-SPECIFIC ADENOSINE ON THE 28S rRNA.		FT SIGNAL 1 25 POTENTIAL.
CC	-!- C-SPECIFIC ADENOSINE ON THE 28S rRNA.		FT CHAIN 26 297 RIBOSOME INACTIVATING PROTEIN, A CHAIN.
CC	-!- C-SPECIFIC ADENOSINE ON THE 28S rRNA.		FT CHAIN 298 563 RIBOSOME INACTIVATING PROTEIN, B CHAIN.
CC	-!- C-SPECIFIC ADENOSINE ON THE 28S rRNA.		SQ SEQUENCE 563 AA; 62336 MW; 3ED2BCC0BE796205 CRC44;
DR	InterPro; IP0001574; RIP.		Query Match 33.8%; Score 329.5; DB 10; Length 563;
DR	Pfam; PF00161; RIP; 1.		Best Local Similarity 40.5%; Pred. No. 7.5e-23;
DR	PRINTS; PR00396; SHIGARICIN.		Matches 77; Conservative 37; Mismatches 51; Indels 25; Gaps 5;
DR	PROSITE; PS00275; SHIGA_RICIN; 1.		DR InterPro; IP0001574; RIP.
KW	Hydrolase; Toxin.		DR YPSVSEFNLAGAKSATRDPFLKQNRKTYVPLRRESEVOYKNRFVLLVNY 87
SQ	SEQUENCE 289 AA; 31650 MW; 286AC14D48BCA175 CRC64;		Db 28 YPSVSEFNLAGAKSATRDPFLKQNRKTYVPLRRESEVOYKNRFVLLVNY 87
Query Match	34.1%; Score 332; DB 10; Length 289;		QY 57 AEISVTLALDVTVNAYVVGYRAGNSAYFFPDNQDEAII--THLFDTQNRTPAFGGNY 114
Best Local Similarity	38.9%; Pred. No. 1.7e-23;		Db 88 NGNTVTLADVTNLVYVVAFSANANSYFF---KDQLQKSNLVFGVR-QHTLPFGNY 141
Matches	72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;		QY 115 DRLEQAGNLRENLELGNGPLEFAISALAYYSTGTQPLTLSFICIQMISEAARRQY 174
Qy	10 INFITAGATQSYNTNFIRAVGRGTVLPN-----RVLPIQNRFVLEVSINHAEL		Db 142 DNLETAAGTPTRESTELGSPSPDGAITSLYDE-----SVARSLVVQTMVSEAAFRY 194
Db	25 VSERLSGATSSSYGVFISNLR--KALPNERKLYDIPLRSLSLPSQRVALVHLTNAYDE		QY 175 IEGERMRTTR 184
Qy	60 SYTVALDVTNYVYVYRAGNSAYFFPDNQDEA--DAITHLFTDVQNRTPAFGGNYDRLE		Db 195 IEQEVRRSLQ 204
Db	82 TISVALIDTVNYVYRAGDTSYFF--NEASATEAKVYFKDSMRKTFIPLPSGNYERLQ		RESULT 9
Qy	119 QLAGNLRLENLGNGLPPEEAISALAYYYSTGGTQLPTLARSLFICIQMISSEAARYIEEG		OQLR3 PRELIMINARY;
Db	139 TAAGKIRENTIPGLPALSATITLEYYNAN----SAASALMVLQSTSSEAARYKFIQQ		AC OQLR3 PRELIMINARY;
Qy	179 MRTRI 183		DT 01-OCT-2000 (TREMBLrel. 15, Created)
Db	194 IGKV 198		DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
RESULT 8			DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
AC	O04367;	PRELIMINARY;	DE Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
DT	01-JUL-1997 (TREMBLrel. 04, Created)		GN TBK.
DT	01-OCT-1997 (TREMBLrel. 04, Last sequence update)		OS Trichosanthes sp. Bac Kan 8-98.
DB	Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA N-glycosidase).		OC Eukaryota; Viridiplante; Streptophyta; Embryophyta; Tracheophyta;
Qy			OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Db			OC eurosidids I; Cucurbitales; Cucurbitaceae; Trichosanthes .
RN			NCBI_TaxID=118182;
RP			[1]
Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;			SEQUENCE FROM N.A.
"Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoc)." ;			RA
Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			RT

CC - CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
SPECIFIC ADENOSINE ON THE 28S RNA.

CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

DR EMBL: AB03934; BAA9250.1; -.

DR HSSP: P0989; IMRJ.

DR InterPro: IPR001574; RIP.

DR Pfam: PF00165; RIP; 1.

DR PRINTS: PR00396; SHIGARICIN.

DR Hydrolyse; Toxin.

KW Hydrolyse; Toxin.

FT NON\_TER 1 1

FT NON\_TER 247 247

SQ SEQUENCE 247 AA; 27199 MW;

Query Match 10 INFITAGATVQSYTNFIRAVR ---GRLTULP-NRVLGLPNQRFLIVLNHAEELSVT 62  
Best Local Similarity 33.4%; Score 326; DB 10; Length 247;  
Matches 72; Conservative 44; Mismatches 50; Indels 16; Gaps 5;

Qy 63 LADDDTNAVYVGYRAGNSAYFFHDNQEDA-EAHTLFTDVNRYTFAFGNYDRLEQLA 121  
Db 62 VADVTNTVYVGMGRAGDTSYF--NEASATEAKTYFKDAKRVTLPSGNYERLQIAA 118

Qy 122 GNLRNIELNGGLEEATSALEYSTGTQPLTLLARSLICOMISEAAREFYIEGMR 181  
Db 119 GKIRENPIGLPADSAITLTFTYNAN ---SAASALMVLQSTSEARYTFEQIGK 173

Qy 182 RI 183

Db 174 RV 175

RESULT 10

Q9AVR2 PRELIMINARY; PRT; 564 AA.

AC Q9AVR2; PRT; 564 AA.

DR 01-JUN-2001 (TREMBLrel. 17, Created)  
01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DR 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA  
DE N-glycosidase).

GN Sambucus ebulus.

OS Sambucus ebulus.

OC Spermatophytina; Streptophytina; Embryophytina; Tracheophytina;  
OC core eudicots; Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.

OX NCBI\_TaxID:28503;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Leaf;

RA Gibres T., Iglesias R., Perez Y., Ferreras J.M., Cidores L.;  
RT Molecular cloning of ebulin 1";  
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

CC - CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
SPECIFIC ADENOSINE ON THE 28S RNA.

CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

DR EMBL: AJ408822; CAC3178.1; -.

DR HSSP: P02819; 2AAI.

DR InterPro: IPR000772; Ricin\_B\_lectin.

DR Pfam: PF00652; Ricin\_B\_lectin; 6.

DR PRINTS: PR00396; SHIGARICIN.

DR SMART: SM00458; RICIN\_2.

DR PROSITE: PS00231; RICIN\_B\_LECTIN; 2.

DR PROSITE: PS00275; SHIGA\_RICIN; 1.

RW Glycosidase; Hydrolase; Signal; Toxin.

FT SIGNAL 1 25  
FT CHAIN 26 298  
FT CHAIN 299 564

SQ SEQUENCE 564 AA; 62694 MW; 8261681A6DB55CB8 CRC64;

Query Match 33.2%; Score 323.5; DB 10; Length 564;  
Best Local Similarity 40.0%; Pred. No. 2.8e-22; Mismatches 51; Indels 25; Gaps 6;

Qy 7 YPTINFTAGATVQSYTNFIRAVRGR ---ITVLPNRVGLPINQRFLIVLNH 56  
Db 28 YPVVSFNLAGKSTTYDFKLNLDRDTATGTYEVNGLPVLRRESEYQVNRLRVLVNTY 87

Qy 57 AELSVTLLDVNAYVVGYRAGNSAYFFPDNQEDAEEA --THLFDTDVNRYTFAFGNY 114  
Db 88 NGDTVTSRASDVNTNLVLSANGNSTFF ---KDTELQSNLFGLT-TQHLSFTGNY 141

Query Match 115 DRBQLAGNLRENTELNGNPLBEIASAUYYETGGTOLPLARSFTCIONSEEARFQY 174  
Best Local Similarity 39.6%; Score 326; DB 10; Length 247;  
Matches 72; Conservative 44; Mismatches 50; Indels 16; Gaps 5;

Qy 175 IECEMRTR 184  
Db 142 DNLETAAGTRRESIELGPNPDLGAIITSWY--DGG---VARSLLVLQVPEARRFRY 194

Qy 195 IEQEVRRSLQ 204

RESULT 11

Q06076 PRELIMINARY; PRT; 528 AA.

AC Q06076; PRT; 528 AA.

DR 01-NOV-1996 (TREMBLrel. 01, Created)  
DR 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DR 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Abrin-d (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).

OS Abrus precatorius (Indian licorice) (Crab's eye).

OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;  
OC Spermatophytina; Magnoliophytina; eudicots; core eudicots; Rosidae;  
OC euRosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.

NCBI\_TaxID:3816;

RN [1]

RP SEQUENCE FROM N.A.

DR MEDLINE-93132798; PubMed-8421313;

RA Hung C.-H., Lee M.-C., Lin J.-Y., Lee T.-C., Lin J.-Y.

RT "Primary structure of three distinct isoabrinins determined by cDNA sequencing, conservation and significance.";  
RL J. Mol. Biol. 229:263-267 (1993).

CC - CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
SPECIFIC ADENOSINE ON THE 28S RNA.

CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

DR EMBL: M98346; AAA32626.1; -.

DR HSSP: P11140; 1ABP

DR InterPro: IPR000772; Ricin\_B\_lectin.

DR Pfam: PF00652; Ricin\_B\_lectin; 6.

DR PRPRINTS; PR00396; SHIGARICIN.

DR SMART; SM00458; RICIN\_2.

DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.

DR PROSITE; PS00275; SHIGA\_RICIN; 1.

KW Hydrolase; Toxin.

FT NON\_TER 1 1

FT NON\_TER 528 528

SQ SEQUENCE 528 AA; 58870 MW; 62ED42FBFFF60F8 CRC64;

Query Match 32.7%; Score 318.5; DB 10; Length 528;

Best Local Similarity 43.3%; Pred. No. 7.7e-22; Mismatches 69; Indels 15; Gaps 4;

Qy 6 QYPLINFTAGATVQSYTNFIRAVRGR ---VLPNRVGLPINQRFLIVLNH 57  
Db 1 QDQVTKFTEGATOSYKQFTEALQRQLGLIHDIPVLPDPTTVEERNRYTIVLNH 60

Qy 58 ELSVTLLDVNAYVVGYRAGNSAYFFPDNQEDAEEAITHLFTDVNRYTFAFGNYDRL 117

Db 61 RESTIEVGDVNTNAYVVGYRAGSQSFLL--RDAPRSASSTYLFPGTQ-RVSLRFDSYGD 116

Qy	118 EQLAGNLRENTIELNGNPLEEAIASALYYSTGGTQLPLTALARSHIQTOMISAAFRQYIEG	177	OS Abrus precatorius (Indian licorice) (Crab's eye). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreia; Abrus.
Db	117 ERWAHQTRBEEISLGLQALTHAIS---PLRSGASNDERKARTLIVITIQMASSEARYTCISN	173	OX NCBI_TAXID:3816; RN [1] RP SEQUENCE FROM N.A. RC TISSUE=LEAF;
Qy	178 EMTRIR 184		RX MEDLINE=91201329; PubMed=2016300; RA Evensen G.; Mathiesen A.; Sundan A.
Db	174 RVEVSIR 180		RT "Direct molecular cloning and expression of two distinct abrin A- chains."; RL J. Biol. Chem. 266:6848-6852 (1991).
RESULT 1.2			
Q8LPV7	PRELIMINARY;	PRT;	270 AA.
ID Q8LPV7;			
AC Q8LPV7;			
DT 01-OCT-2002 (TREMBLrel. 22, Created)			
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase)			
DE (Fragment)			
GN TCS.			
OS Trichosanthes kirilowii (Mongolian snake-gourd).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;			
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthaceae;			
OX NCBI_TAXID=3677;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Yuan H., Wang Y., Liu T., An C., Chen Z.,			
RT Trichosanthes kirilowii trichosanthin precursor (TCS) gene. ";			
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE			
CC SPECIFIC ADENOSINE ON THE 28S RNA.			
CC -!- SIMILARITY: BELONGS TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING PROTEINS. BELONGS TO TYPE 2 RIP.			
DR EMBL: AY082348; AACM22782.1; -.			
DR InterPro; IPR001574; RIP.			
DR PR00161; RIP; 1.			
DR PRINTS; PR00396; SHIGARICIN.			
DR PROSITE; PS00275; SHIGA_RICIN.			
DR Hydrolease; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.			
FT CHAIN 24 >270 MW; BBFCB46B9E92B5DE CRC64;			
FT NON TER 270 AA; 29683 MW; 531713B754F9B769 CRC64;			
SQ SEQUENCE 270 AA; 29683 MW;			
Query Match 14			
Q945S2	PRELIMINARY;	PRT;	563 AA.
ID Q945S2;			
AC Q945S2;			
DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE Ribosome-inactivating protein (EC 3.2.2.22) (rRNA AVL).			
GN Sambucus nigra (European elder).			
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;			
OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.			
RESULT 13			
Q38760	PRELIMINARY;	PRT;	252 AA.
ID Q38760;			
AC Q38760;			
DT 01-NOV-1998 (TREMBLrel. 08, Created)			
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DE Abrin-E (rRNA N-glycosidase) (EC 3.2.2.22) (Fragment).			
GN RIP.			

OX NCBI\_TaxID=4202;  
 RN [1] SEQUENCE FROM N.A.  
 RP TISSUE=Leaf;  
 RC  
 RA Van Damme E.J.M.;  
 RT Characterization and cloning of lectins and ribosome-inactivating  
 proteins from *Sambucus nigra* leaves";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.  
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL; AF40935; AAL04123.1;  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP\_Efam; P00052; Ricin\_B\_lectin; 6.  
 DR InterPro; IPR00161; RIP; I.  
 DR PRINTS; PRO0396; SHIGARICIN.  
 DR SMART; SMART; SMO0458; RICIN.  
 DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Hydrolase; Toxin.  
 SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDC33BF10 CRC64;

Query Match 31.5%; Score 307.5; DB 10; Length 563;  
 Best Local Similarity 38.4%; Pred. No. 9.5e-2; Indels 25; Gaps 5;  
 Matches 73; Conservative 36; Mismatches 56;

Qy 7 YPLINPFTAGATQSYTNFIRAVR-----GRILTVLPNRVGLPQNQFILVELSNH 56  
 Db 28 YPSVSEFLDGAKSATYRDFLSNLRKTVATGTYEVNGIPLVRLRESEYQVKSRFLVPLTNY 87

Qy 57 AELSVTIALDVNAYYVGAGRNSAYFFHPDQEAAI--THLFTDVQNYTFAFGNY 114  
 Db 88 NGNTVILAVDVLNLYVAFSGMANSYF----KDAEVQKSNLFGTKQN-TLSFTGNY 141

Qy 115 DRLEQLAGNLRENIELGNGPLFEAISALYYSTGGTOLPLTLARSFLICIONMSEARFQY 174  
 Db 142 DNLETAANTRRSELGSPSLDGAITSLYHGD-----SVRSLLVIVQWSEARFRY 194

Qy 175 IEGEMTRIR 184  
 Db 195 IEQEVRRSLQ 204

**RESULT 15**

Q8GT32 PRELIMINARY; PRT; 563 AA.  
 ID Q8GT32  
 AC Q8GT32;  
 DT 01-MAR-2003 (T-EMBL; 23, Created)  
 DT 01-MAR-2003 (T-EMBL; 23, Last sequence update)  
 DT 01-MAR-2003 (T-EMBL; 23, Last annotation update)  
 DE Type 2 ribosome-inactivating protein nigrin 1 precursor  
 DE (EC 3.2.2.22).  
 OS *Sambucus nigra* (European elder).  
 OC Spermatophytidae; Streptophytidae; Embryophytidae; Tracheophytidae;  
 OC Asteridae; campanulids; Dipsacales; Asterales; core eudicots;  
 OC Asteridae; campnulids; Dipsacales; Asteraceae; Sambucus.  
 OX NCBI\_TaxID=4202;  
 RN [1] SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RA Girbes T., Arias F.J., Antolin P.;  
 RT Characterization and molecular cloning of Nigrin 1, a type two  
 ribosome-inactivating protein from leaves of elder (*Sambucus nigra*).";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF242280; AAN8130.1; -.  
 KW Hydrolase; Glycosidase.  
 SQ SEQUENCE 563 AA; 62173 MW; 0EB236421FC5E04F CRC64;

Query Match 31.5%; Score 307.5; DB 10; Length 563;  
 Best Local Similarity 38.4%; Pred. No. 9.5e-2; Indels 25; Gaps 5;  
 Matches 73; Conservative 36; Mismatches 56;